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**Morley**

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(54) **METHOD FOR DNA BREAKPOINT ANALYSIS**

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C12Q 1/68 (2006.01)

(52) **U.S. Cl.**

CPC ..... C12Q 1/6858 (2013.01)

(58) **Field of Classification Search**

USPC ..... 435/6, 91.2

See application file for complete search history.

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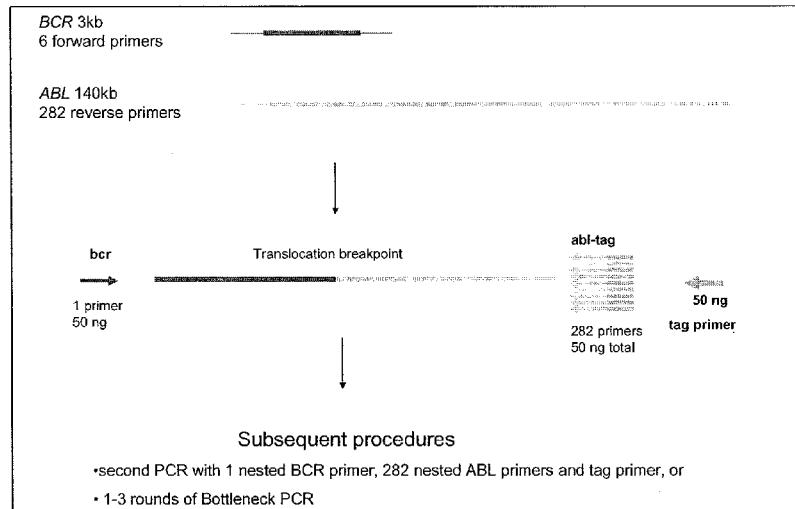
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(57) **ABSTRACT**

The present invention relates to a method for identifying a DNA breakpoint and agents for use therein. More particularly, the present invention provides a method for identifying a gene translocation breakpoint based on the application of a novel multiplex DNA amplification technique. The method of the present invention facilitates not only the identification of the breakpoint position but, further, enables the isolation of the DNA segment across which the breakpoint occurs. This provides a valuable opportunity to conduct further analysis of the breakpoint region, such as to sequence across this region. The method of the present invention is useful in a range of applications including, but not limited to, providing a routine means to characterize the gene breakpoint associated with disease onset in a patient and thereby enable the design of patient specific probes and primers for ongoing monitoring of the subject disease condition. In addition to monitoring the progression of a condition characterized by the existence of the breakpoint, there is also enabled assessment of the effectiveness of existing therapeutic drugs and/or new therapeutic drugs and, to the extent that the condition is a neoplasm, prediction of the likelihood of a subject's relapse from a remissive state.

**11 Claims, 8 Drawing Sheets**

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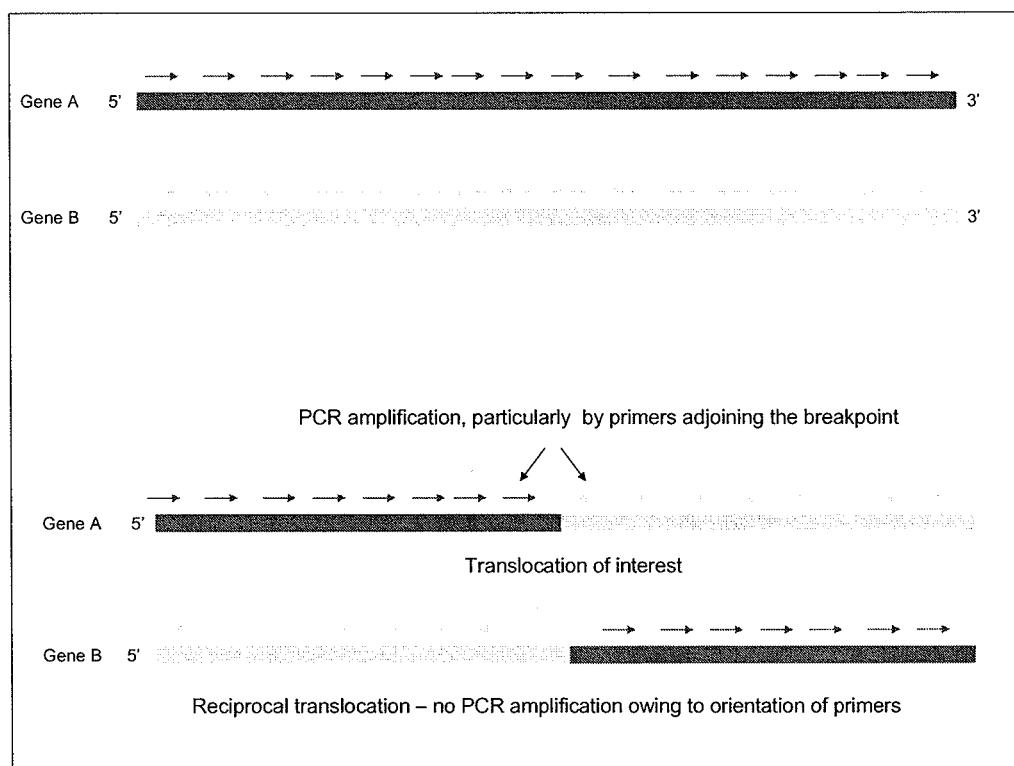
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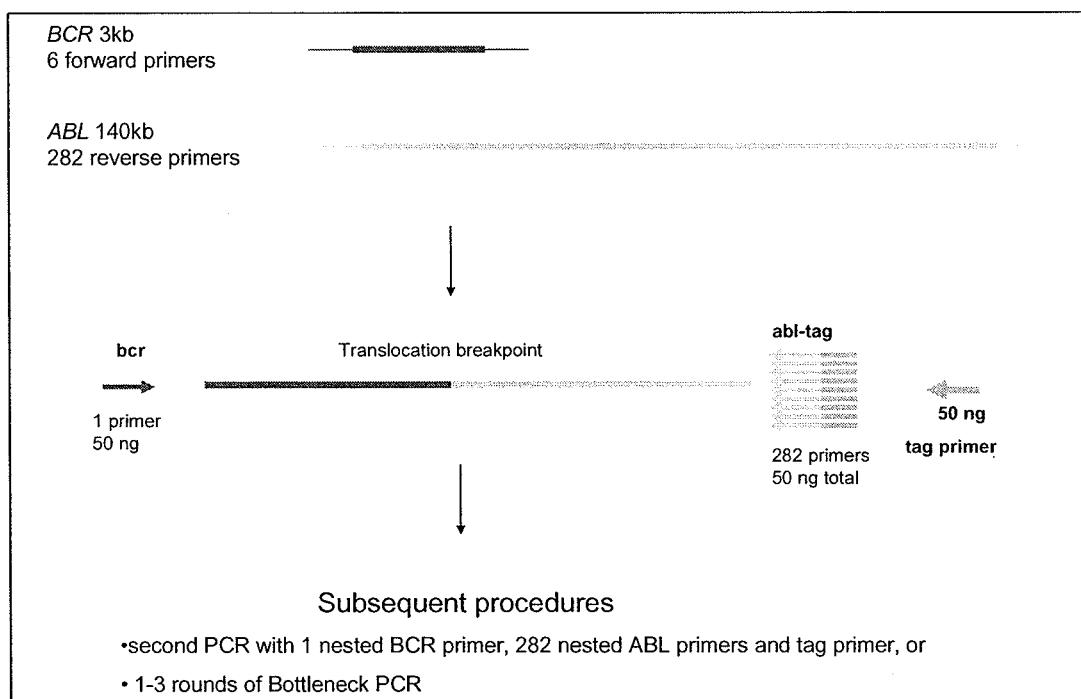
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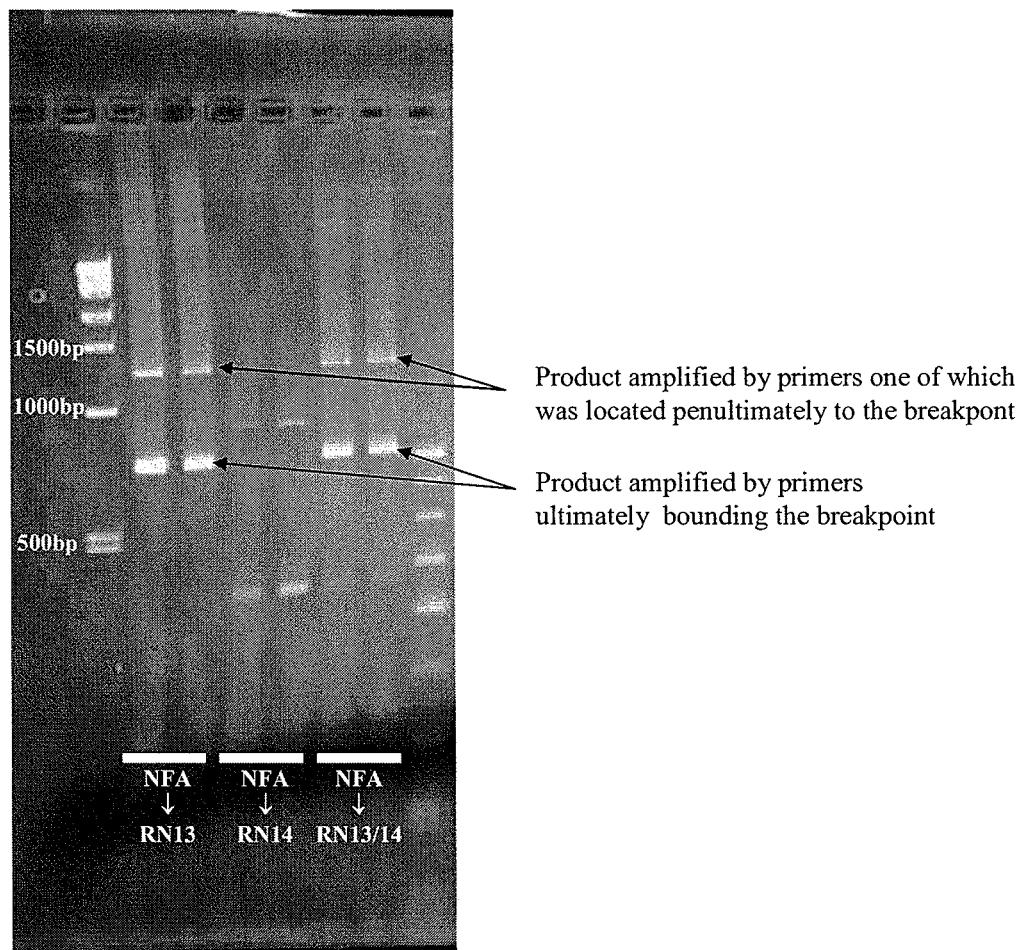
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**FIGURE 1**

## FIGURE 2



**FIGURE 3**

## FIGURE 4

### Patient 1 – GS

gtggggccccccgttccgtg  
123721 tacagggcacctgcagggagggcaggcagctagcctgaaggctgatcccccttcctgtt  
123781 agcaactttgtatggactagtggactttggttcagaaggaagagctatgcttgtagggc  
123841 ctcttgcctcccaggagtggacaagggtgggtaggagcagttctccctgagtggct  
123901 gc\* <-BCR ABL-> \*caccacgtctggctaa  
55621 ttttgtattttagtagagatggggttcaacatgttagccaggctggtctcgaaactcc  
55681 tgacctcaggtgatccacccgcctggccctccaaagtgcgtggattacaggcaggagcc  
55741 actgtgcccggcctgacctcatattgaataccgagtttagttctggaggagctgcagg  
55801 ttttatgaaaaggaaacacatttgattcctcagagcagccacaggccagctctctaagt  
55861 aaagtgcacgtgtcatgtgtgcacactcacacacacgtacacacacattcacaaata  
55741 actgtgcccggcctgacctcatattgaataccgagtttagttctggaggagctgcagg

### Patient 3 – ME

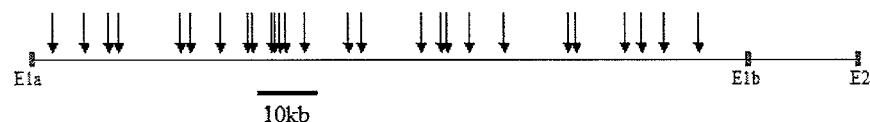
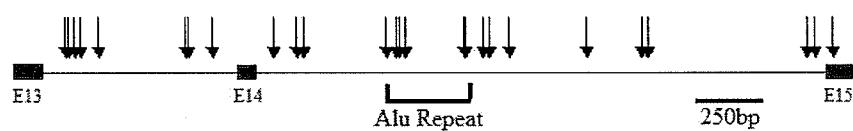
125041 tttgggaggctgaggcagggtggatcgcttgcggctcaggagttggagaccagcctgaccaa  
125101 catggtaaaaccctgtgtctactaaaaatacaaagattagccggctaggcagtggcac  
125161 ctgtaatcacaactgcctggaggctgagggaaagagaatcgcttgcacccaggaggcgg  
125221 ggtgcagtgagccgagcttgcactgcattccagcctggcgacagag\* <-BCR  
ABL-> \*ggtctcact  
28981 ctgttgaactcctggctcaaggatcctcctacctcgccctcacaaggatattggaa  
29041 ttacaggtgtgagtcactgcagctggccttacttactgtgaggagtaaacagactgc  
29101 atggtggcttaatgccatctaacacgagtgactccatgttcagacagtaggatcacaaa  
29161 tgattattatataaatgaaatggccacaggtacatagactaaggagccacatccctgct

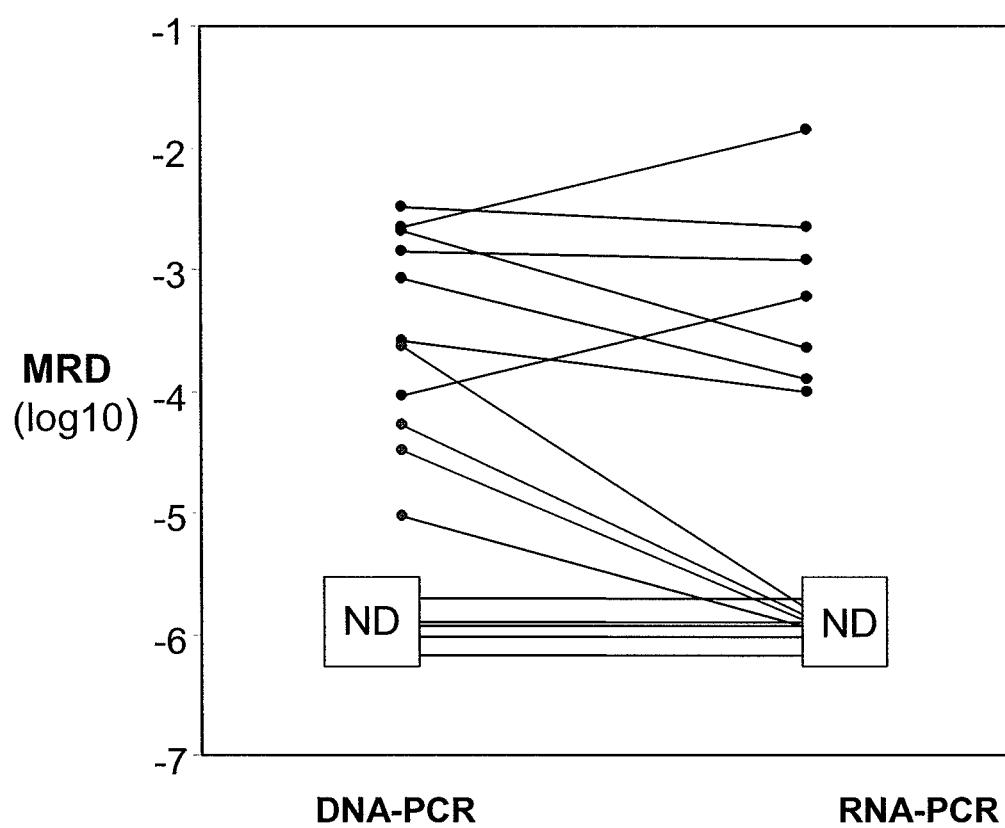
**Figure 4 (cont'd)****Patient 5 – AB**

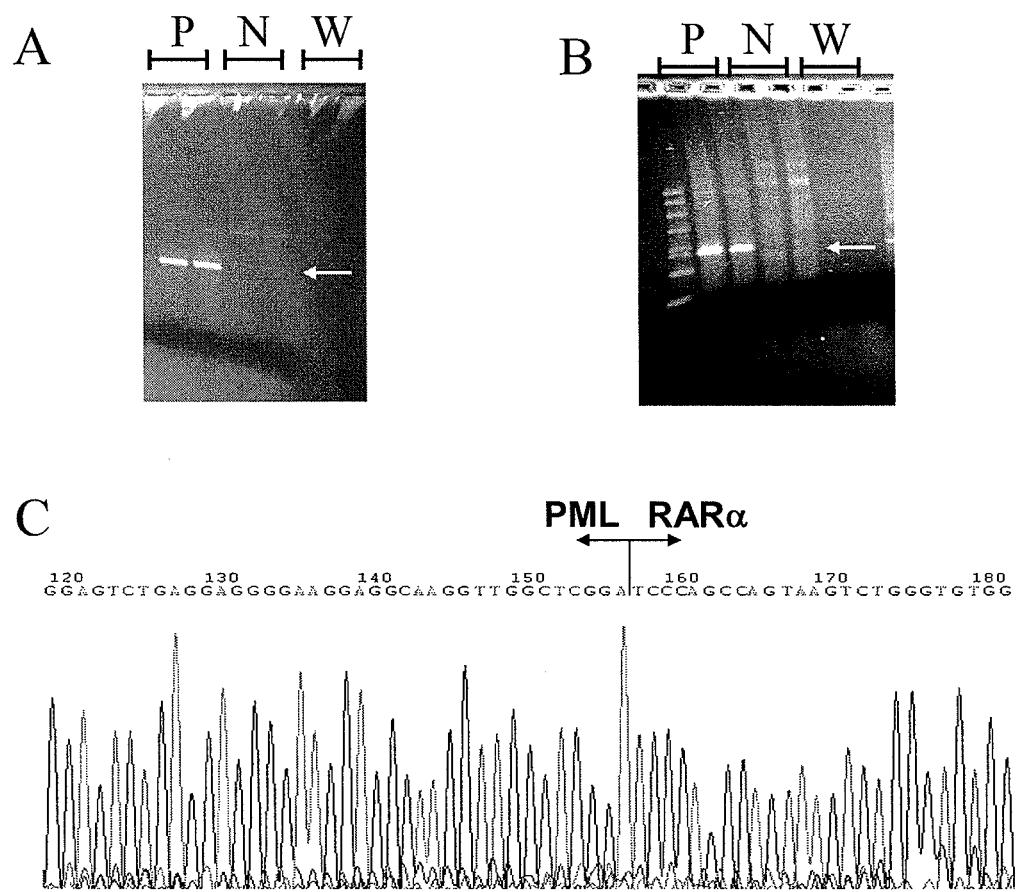
124021 cctccagctacacctggcagccggactttggtaagctgtttgcattcactgttcaca  
124081 tatgctcagtcacacacacacagcatacgctatgcacatgtgtccacacacacccccacccac  
124141 atcccacatcaccccgacccctctgctgtccttggAACCTTATTACACTCGAGTCACT  
124201 ggTTGCTGTATTGTGAAACCAGCTGGATCC\* <- BCR  
*ABL ->* \*ttatttataacaacatttc  
94081 agcgtggcaactgcagttcagaatggtggaaattataccagttagagagatgcaaatg  
94141 attaaaataggaagaaggcagggtgtctggcccagaggaccagattaagaagacccatg  
94201 agagttacaatagtttagtggaaatggcttgcaaacctcatgtctacagaagctgg

**Patient 6 – CH**

125521 tgcacccataacataatcttcctggccctgtctggctgcctataaacgct  
125581 ggtgttccctcggtggccctccctgcattccctgcattctcccccgggtctgtgag  
125641 caatacagcgtgacaccctacgctgccccgtggtcccccgttgtctccctgcctccc  
125701 tgTTACCTTCTTCTATCTTCTTGCCCCG\* <- BCR  
*ABL ->* \*gtgagctccgc  
81961 ctccgtcagatcagtggccgcattagttctcataggagcatgaaatctattgtgaaca  
82021 gtacatgcgtggatccaggttgcgtgccttagtgagaatctaattgcctgaggatct  
82081 cattgtctttatcactccagataggactgtctagttgcaggaaaacaagctcagggt  
82141 cccactgattctacattacagtgggtgtataatttatattacaatgtaaaaataaa

**Figure 5****A) ABL****B) BCR**

**Figure 6**

**Figure 7**

## METHOD FOR DNA BREAKPOINT ANALYSIS

### CROSS REFERENCE TO RELATED APPLICATION

This application claims the benefit and priority to International Application No. PCT/AU2008/000779; filed May 30, 2008, which designated the United States and was published in English and claims the benefit of priority to U.S. Provisional No. 60/941,419, filed Jun. 1, 2007. The disclosures of the above-referenced applications are hereby expressly incorporated by reference in their entirieties.

### SEQUENCE LISTING

The present application is being filed along with a Sequence Listing in electronic format. The Sequence Listing is provided as a file entitled DAVI332\_001APC.TXT, created May 30, 2008, which is 91 Kb in size. The information in the electronic format of the Sequence Listing is incorporated herein by reference in its entirety.

### FIELD OF THE INVENTION

The present invention relates to a method for identifying a DNA breakpoint and agents for use therein. More particularly, the present invention provides a method for identifying a gene translocation breakpoint based on the application of a novel multiplex DNA amplification technique. The method of the present invention facilitates not only the identification of the breakpoint position but, further, enables the isolation of the DNA segment across which the breakpoint occurs. This provides a valuable opportunity to conduct further analysis of the breakpoint region, such as to sequence across this region. The method of the present invention is useful in a range of applications including, but not limited to, providing a routine means to characterise the gene breakpoint associated with disease onset in a patient and thereby enable the design of patient specific probes and primers for ongoing monitoring of the subject disease condition. In addition to monitoring the progression of a condition characterised by the existence of the breakpoint, there is also enabled assessment of the effectiveness of existing therapeutic drugs and/or new therapeutic drugs and, to the extent that the condition is a neoplasm, prediction of the likelihood of a subject's relapse from a remissive state.

### BACKGROUND OF THE INVENTION

The reference in this specification to any prior publication (or information derived from it), or to any matter which is known, is not, and should not be taken as an acknowledgment or admission or any form of suggestion that that prior publication (or information derived from it) or known matter forms part of the common general knowledge in the field of endeavour to which this specification relates.

Bibliographic details of the publications referred to by author in this specification are collected alphabetically at the end of the description.

Chromosomal translocations bring the previously unlinked segments of the genome together by virtue of the exchange of parts between non-homologous chromosomes. Although some translocations are not associated with a new phenotype, others may result in disease due to the modulation of protein expression or the synthesis of a new fusion protein.

There are two main types of chromosomal translocations which occur, these being reciprocal translocations (also known as non-Robertsonian) and Robertsonian translocations. Further, translocations can be balanced (in an even exchange of material with no genetic information extra or missing) or unbalanced (where the exchange of chromosome material is unequal resulting in extra or missing genes).

10 Reciprocal (non-Robertsonian) translocations usually result in an exchange of material between non-homologous chromosomes and are found in about 1 in 600 newborns. Such translocations are usually harmless and may be found through prenatal diagnosis. However, carriers of balanced reciprocal translocations exhibit an increased risk of creating gametes with unbalanced chromosome translocations thereby leading to miscarriages or children with abnormalities.

15 Robertsonian translocations involve two acrocentric chromosomes that fuse near the centromere region with loss of the short arms. The resulting karyotype has only 45 chromosomes since two chromosomes have fused together. Robertsonian translocations have been observed involving all combinations of acrocentric chromosomes. The most common translocation involves chromosomes 13 and 14 and is seen in about 1 in 1300 persons. Like other translocations, carriers of 20 Robertsonian translocations are phenotypically normal, but exhibit a risk of unbalanced gametes which lead to miscarriages or abnormal offspring. For example, carriers of Robertsonian translocations involving chromosome 21 exhibit a higher probability of having a child with Down syndrome.

25 Diseases which may result from the occurrence of a translocation include:

- (i) Cancer—several forms of cancer are caused by translocations; this mainly having been described in leukemia (eg. acute myelogenous leukemia and chronic myelogenous leukemia).
- (ii) Infertility—this can occur where one of the would-be parents carries a balanced translocation, where the parent is asymptomatic but conceived foetuses are not viable.
- (iii) Down syndrome—in some cases this is caused by a Robertsonian translocation of about a third of chromosome 21 onto chromosome 14.

30 Specific examples of chromosomal translocations and the disease with which they are associated include:

- t(2;5)(p23;q35)—anaplastic large cell lymphoma
- t(8;14)—Burkitt's lymphoma (c-myc)
- t(9;22)(q34;q11)—Philadelphia chromosome, CML, ALL
- t(11;14)—Mantle cell lymphoma (Bcl-1)
- t(11;22)(q24;q11.2-12)—Ewing's sarcoma
- t(14;18)(q32;q21)—follicular lymphoma (Bcl-2)
- t(17;22)—dermatofibrosarcoma protuberans
- t(15;17)—acute promyelocytic leukemia (pml and retinoic acid receptor genes)
- t(1;12)(q21;p13)—acute myelogenous leukemia
- t(9;12)(p24;p13)—CML, ALL (TEL-JAK2)
- t(X;18)(p11.2;q11.2)—Synovial sarcoma
- t(1;11)(q42.1;q14.3)—Schizophrenia
- t(1;19)—acute pre-B cell leukemia (PBX-1 and E2A genes).

35 The shorthand t(A;B)(p1;q2) is used to denote a translocation between chromosome A and chromosome B. The information in the second set of parentheses, when given, gives a precise location within the chromosome for chromosomes A and B respectively—with p indicating the short arm of the chromosome, q indicating the long arm, and the numbers of p and q refers to regions, bands and sub-bands seen when staining the chromosomes under microscope.

As detailed above, chronic myelogenous leukemia is an example of a neoplastic condition which is caused by a chromosomal translocation. However, unlike many neoplastic conditions, its treatment prospects are quite good if it can be effectively diagnosed and monitored.

In virtually all cases of chronic myelogenous leukemia, a specific translocation is seen. This translocation involves the reciprocal fusion of small pieces from the long arms of chromosome 9 and 22. The altered chromosome 22 is known as the Philadelphia chromosome (abbreviated as Ph1). When the breakpoint of the Ph1 chromosome was sequenced, it was found that the translocation creates a fusion gene by bringing together sequences from the c-ABL proto-oncogene and another BCR (breakpoint cluster region). The BCR-ABL fusion gene encodes a phosphoprotein (p210) that functions as a dysregulated protein tyrosine kinase and predisposes the cell to become neoplastic. This hypothesis is supported by finding that expression of p210 results in transformation of a variety of hematopoietic cell lines in vitro and that mice transgenic for the human BCR-ABL gene develop a number of hematologic malignancies.

Another well studied example of a translocation generating cancer is seen in Burkitt's lymphoma. In some cases of this B cell tumor, a translocation is seen involving chromosome 8 and one of three other chromosomes (2, 14 or 22). In these cases, a fusion protein is not produced. Rather, the c-myc proto-oncogene on chromosome 8 is brought under transcriptional control of an immunoglobulin gene promoter. In B cells, immunoglobulin promoters are transcriptionally quite active, resulting in over expression of c-myc, which is known from several other systems to exhibit monogenic properties. Accordingly, this translocation results in aberrant high expression of an oncogenic protein.

The classical method of diagnosing chromosomal translocations, such as those observed in chronic myelogenous leukemia, is by karyotyping. For many translocations, however, it is now possible to detect the translocation by PCR, using primers which span the breakpoint. In some cases, the PCR technique can also be used for sensitive detection and monitoring of treatment. Monitoring to determine the effect of treatment has become increasingly important for diseases such as chronic myeloid leukemia and acute promyelocytic leukemia as increasingly effective treatment has been developed. For monitoring in these 2 diseases, the starting material for the PCR is RNA. The translocation breakpoint is within the introns of the respective genes and, as a consequence, RNA splicing removes the sequence of RNA transcribed by introns and results in only one or a very limited number of final mRNA products being produced, despite the very large number of different translocations which are present in the patient population.

However, the use of RNA as the starting material to detect and quantify the translocation by PCR suffers the disadvantage that RNA is a difficult molecule to work with due to its inherent susceptibility to degradation. DNA is a more stable molecule. However, the initial identification and characterisation of the breakpoint in the context of DNA is much more difficult since cluster regions of chromosomal fusion sites often span large introns of several tens of thousands of nucleotides. These sizes are too large for direct coverage by a single PCR reaction. There therefore exists an ongoing need to develop means for routinely conducting breakpoint analyses on DNA samples.

In work leading up to the present invention, a novel multiplex amplification reaction has been developed which enables the localisation and analysis of a breakpoint in a DNA sample. Despite the precise position of the breakpoint being

unknown, the method of the present invention nevertheless enables diagnosis of the existence of the breakpoint in a DNA sample and the isolation and analysis of the breakpoint region using a relatively modest and simple multiplex amplification reaction. The design of this amplification reaction results in the advantage that generation of long PCR products is not required. Still further, the optional incorporation of a primer hybridisation tag region at the 5' end of the amplification primers enables the rapid generation of large copy numbers of the amplicons generated using these primers and therefore facilitates the isolation and analysis of the amplicons.

#### SUMMARY OF THE INVENTION

Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integers or steps.

As used herein, the term "derived from" shall be taken to indicate that a particular integer or group of integers has originated from the species specified, but has not necessarily been obtained directly from the specified source. Further, as used herein the singular forms of "a", "and" and "the" include plural referents unless the context clearly dictates otherwise.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

The subject specification contains nucleotide sequence information prepared using the programme PatentIn Version 3.1, presented herein after the bibliography. Each nucleotide sequence is identified in the sequence listing by the numeric indicator <210> followed by the sequence identifier (eg. <210>1, <210>2, etc). The length, type of sequence (DNA, etc) and source organism for each sequence is indicated by information provided in the numeric indicator fields <211>, <212> and <213>, respectively. Nucleotide sequences referred to in the specification are identified by the indicator SEQ ID NO: followed by the sequence identifier (eg. SEQ ID NO: 1, SEQ ID NO:2, etc.). The sequence identifier referred to in the specification correlates to the information provided in numeric indicator field <400> in the sequence listing, which is followed by the sequence identifier (eg. <400>1, <400>2, etc). That is SEQ ID NO:1 as detailed in the specification correlates to the sequence indicated as <400>1 in the sequence listing

One aspect the present invention is directed to a method of identifying a gene breakpoint, said method comprising:

- (i) contacting a DNA sample with:
  - (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;

## 5

- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:

- (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
- (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the other reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

The present invention therefore preferably provides a method of identifying a chromosomal gene translocation breakpoint, said method comprising:

- (i) contacting a genomic DNA sample with:

- (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

- (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;

- (ii) amplifying the DNA sample of step (i);

- (iii) optionally contacting the amplicon generated in step (ii) with:

- (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

- (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which

## 6

- forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

There is therefore preferably provided a method of identifying a gene breakpoint, said method comprising:

- (i) contacting a DNA sample with
  - (a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

- (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;

- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:

- (a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

- (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

The present invention therefore provides a method of identifying a gene translocation breakpoint, said method comprising:

- (i) contacting a DNA sample with
  - (a) one to thirty forward primers directed to a DNA region of the antisense strand of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

- (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are

- the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (c) a primer directed to the forward primer oligonucleotide tag of step (i)(a); and
- (d) a primer directed to the reverse primer oligonucleotide tag of step (i)(b);
- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:
- (a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (c) a primer directed to the forward primer oligonucleotide tag of step (iii)(a); and
  - (d) a primer directed to the reverse primer oligonucleotide tag of step (iii)(b);
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

According to this preferred embodiment there is provided a method of identifying a chromosomal BCR-ABL translocation breakpoint, said method comprising:

- (i) contacting a DNA sample with:
- (a) one or more forward primers directed to a DNA region of BCR or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of ABL or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:
- (a) one or more forward primers directed to a DNA region of BCR or fragment thereof, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to ABL or fragment thereof, which primers are directed to DNA

regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

(iv) amplifying the DNA sample of step (iii);

(v) analysing said amplified DNA.

The present invention therefore preferably provides a method of identifying a chromosomal BCR-ABL translocation breakpoint, said method comprising:

- (i) contacting a DNA sample with:
- (a) one to thirty forward primers directed to a DNA region of BCR or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) twenty-four to four hundred reverse primers directed to a DNA region of ABL or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (c) a primer directed to the forward primer oligonucleotide tag of step (i)(a); and
- (d) a primer directed to the reverse primer oligonucleotide tag of step (i)(b);
- (ii) amplifying the DNA sample of step (i);
- (iii) contacting the amplicon generated in step (ii) with:
- (a) one to thirty forward primers directed to a DNA region of BCR or fragment thereof, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) twenty-four to four hundred reverse primers directed to a DNA region of ABL or fragment thereof, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (c) a primer directed to the forward primer oligonucleotide tag of step (iii)(a); and
  - (d) a primer directed to the reverse primer oligonucleotide tag of step (iii)(b);
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) isolating and sequencing said amplified DNA.

## BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1 is a schematic representation of the strategy for amplification of the breakpoint region in the first round PCR. The forward primers for gene A and the reverse primers for gene B are preferably used in pools rather than individually. Only primer pairs which closely straddle the breakpoint will produce efficient amplification. The tags and tag primers are not shown. The strategy for the second round PCR is the same although the forward and reverse primers are just internal to their corresponding primers in the first round. In the case of chronic myeloid leukemia, gene A is the BCR gene and gene B is the ABL gene. Primer binding sites are staggered so that the maximum amplicon size does not exceed 1 kilobase.

FIG. 2 is a schematic representation of a protocol for isolation of the BCR-ABL translocation breakpoint in chronic myeloid leukemia.

FIG. 3 is an image of the results of electrophoresis showing amplified material from study of one patient. NFA was the pool of 6 forward BCR primers and NFA 13 and NFA 14 were 2 pools each containing 12 reverse ABL primers. NFA 13/14 was a pool containing the 24 ABL primers belonging to pools 13 and 14.

FIG. 4 is a representation of the sequences of the breakpoints in 4 patients with chronic myeloid leukemia. The numbers on the left are the Genbank base numbers for the BCR and ABL genes.

FIG. 5 shows the site of the DNA breakpoints in the ABL and BCR genes in the 27 patients with breakpoints isolated and identified. Blue regions in the ABL gene represent the exons 1a, 1b and E2. Red regions in the BCR gene represent exons 13, 14 and 15.

## Isolation of the BCR-ABL Breakpoint in Chronic Myeloid Leukemia (CML)

Samples from 29 CML patients have been studied using the invention. In 27 of these patients the breakpoint sequences have been isolated and detailed sequencing information obtained. For one patient it has not been possible to amplify the BCR/ABL breakpoint. For the remaining patient a suspected breakpoint has been amplified. Sequence information shows the BCR gene at the 5' end and ABL sequence at the 3' end, however this breakpoint has not been confirmed with primers made specifically for the suspected regions.

FIG. 6 is a comparison of DNA-based and RNA-based quantification of minimal residual disease (MRD) in samples of blood from 16 patients with CML. ND=not detected. Y-axis shows the number of leukemic cells as a proportion of total cells. The DNA-based PCR used patient-specific primers synthesised using knowledge of the breakpoint sequence in the patient being studied, the RNA-based PCR was the conventional approach using reverse transcription followed by PCR using generic primers. Black symbols show MRD detected by both techniques, red symbols show disease detected only by DNA-PCR and blue symbols show disease not detected. DNA-based PCR appears to be approximately 2 orders of magnitude more sensitive than RNA-based PCR.

FIG. 7 is an illustration of the isolation of the PML-RAR $\alpha$  breakpoint from a sample from the one patient with acute promyelocytic leukemia

## DETAILED DESCRIPTION OF THE INVENTION

The present invention is predicated, in part, on the determination that gene translocation breakpoints can be routinely and easily identified, via DNA analysis, by sequentially performing two PCR reactions which use multiple primers directed to the genes flanking the breakpoint which are them-

selves tagged at their 5' end with a DNA region suitable for use as a primer hybridisation site. The simultaneous use of multiple primers facilitates the performance of a short PCR, rather than the long PCRs which have been performed to date. By sequentially performing a second PCR using primers directed to gene regions internal to those used in the first reaction, amplification of a DNA molecule spanning the breakpoint region can be achieved in a manner which enables the identification and isolation of a smaller amplification product than has been enabled to date in terms of the analysis of genomic DNA. By incorporating unique tag regions which can themselves be targeted by a primer, amplification of the initial amplicon can be rapidly achieved, thereby overcoming any disadvantage associated with the use of a low concentration of starting primer directed to the genes flanking the breakpoint. The method of the present invention therefore provides a simple yet accurate means of identifying and analysing a gene breakpoint using DNA. To this end, it would be appreciated that although the method of the present invention is exemplified by reference to chronic myelogenous leukemia, this method can be applied to any situation in which a gene breakpoint is sought to be identified via a DNA sample.

Accordingly, in one aspect the present invention is directed to a method of identifying a gene breakpoint, said method comprising:

- (i) contacting a DNA sample with:
  - (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:
  - (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag
    - wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the other reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

## 11

- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

It should be understood that in a preferred embodiment of the present invention, where one primer is used in step (i)(a), it is preferable that two or more primers are used in step (i)(b). The converse applies where one primer is used in step (i)(b). Similarly, in another preferred embodiment, where one primer is used in step (iii)(a), it is preferable that two or more primers are used in step (iii)(b). The converse applies where one primer is used in step (iii)(b).

Reference to the "flanking genes" 5' and 3' to the breakpoint should be understood as a reference to the genes or gene fragments on either side of the breakpoint. In terms of the 5' and 3' nomenclature which is utilised in the context of these genes/gene fragments, this should be understood as a reference to the 5' 3' orientation of the sense strand of double stranded DNA from which the DNA of interest derives. Accordingly, reference to "the flanking gene 5' to the breakpoint" should be understood as a reference to the sense strand of double stranded DNA. To this end, any reference to "gene" or "gene fragment" herein, to the extent that it is not specified, is a reference to the sense strand of double stranded DNA. Reference to the forward primer being directed to the antisense strand of the flanking gene 5' to the breakpoint therefore indicates that the forward primer bears the same DNA sequence as a region of the sense strand 5' to the breakpoint and therefore will bind to and amplify the antisense strand corresponding to that region.

Reference to "gene" should be understood as a reference to a DNA molecule which codes for a protein product, whether that be a full protein or a protein fragment. In terms of chromosomal DNA, the gene will include both intron and exon regions. However, to the extent that the DNA of interest is cDNA, such as might occur if the DNA of interest is vector DNA, there may not exist intron regions. Such DNA may nevertheless include 5' or 3' untranslated regions. Accordingly, reference to "gene" herein should be understood to encompass any form of DNA which codes for a protein or protein fragment including, for example, genomic DNA and cDNA.

Reference to a gene "breakpoint" should be understood as a reference to the point at which a fragment of one gene recombines with another gene or fragment thereof. That is, there has occurred a recombination of two genes such that either one or both genes have become linked at a point within one or both of the genes rather than the beginning or end of one gene being linked to the beginning or end of the other gene. That is, at least one of the subject genes has been cleaved and has recombined with all or part of another gene. The recombination of the two non-homologous gene regions may occur by any method including but not limited to chromosomal gene translocations or in vitro homologous recombinations (such as may occur where a DNA segment is being inserted into a vector or an artificial chromosome or where a vector portion thereof chromosomally integrates in a host cell).

Preferably, the subject gene breakpoint is a chromosomal gene translocation breakpoint. As detailed hereinbefore, chromosomal gene translocations are known to occur and, in some cases, lead to the onset of disease states. Since a gene translocation between two genes will not necessarily result in the breakpoint occurring at precisely the same nucleotide position on the two genes each time the translocation event occurs, it is not possible to assume that the breakpoint position in one patient, such as the Philadelphia chromosome breakpoint in one CML patient, will be the same in another

## 12

patient. The method of the present invention enables the simple yet accurate determination of a gene breakpoint using DNA.

The present invention therefore preferably provides a method of identifying a chromosomal gene translocation breakpoint, said method comprising:

- (i) contacting a genomic DNA sample with:
  - (a) one or more forward primers directed to a DNA region of the flanking gene fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:
  - (a) one or more forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

Reference to "DNA" should be understood as a reference to deoxyribonucleic acid or derivative or analogue thereof. In this regard, it should be understood to encompass all forms of DNA, including cDNA and genomic DNA. The nucleic acid molecules of the present invention may be of any origin including naturally occurring (such as would be derived from a biological sample), recombinantly produced or synthetically produced.

Reference to "derivatives" should be understood to include reference to fragments, homologs or orthologs of said DNA from natural, synthetic or recombinant sources. "Functional derivatives" should be understood as derivatives which exhibit any one or more of the functional activities of DNA. The derivatives of said DNA sequences include fragments having particular regions of the DNA molecule fused to other proteinaceous or non-proteinaceous molecules. "Analogs" contemplated herein include, but are not limited to, modifications to the nucleotide or nucleic acid molecule such as modifications to its chemical makeup or overall conforma-

tion. This includes, for example, modification to the manner in which nucleotides or nucleic acid molecules interact with other nucleotides or nucleic acid molecules such as at the level of backbone formation or complementary base pair hybridisation. The biotinylation or other form of labelling of a nucleotide or nucleic acid molecules is an example of a "functional derivative" as herein defined.

As detailed hereinbefore, the method of the present invention is predicated on the use of multiple oligonucleotide primers to facilitate the multiplexed amplification of a DNA sample of interest. In one embodiment of the present invention, the DNA sample of interest is a hybrid gene which comprises a portion of one gene (gene A) which is located 5' to the translocation breakpoint and a second gene (gene B) which is located 3' to the translocation breakpoint. In a particular embodiment, gene A is BCR and gene B is ABL. The identification of the existence and nature of a gene translocation breakpoint is achieved by using two or more forward primers directed to gene A and two or more reverse primers directed towards gene B. The primers directed to gene A are designed to hybridise at intervals along gene A and the primers directed to gene B are similarly designed to hybridise at intervals along gene B. In the first round PCR, the primers which will amplify the hybrid gene are the upstream primers which hybridise to that portion of gene A which lies 5' to the breakpoint and the downstream primers which hybridise to that portion of gene B which lies 3' to the breakpoint. Furthermore, since small amplicons are amplified more efficiently than larger amplicons, there will occur selection for amplification directed by the primer pair which hybridises closest to the breakpoint. The same principle holds for the second round primers and, since in one embodiment each second round primer corresponds to an individual first-round primer but hybridises internal to it with regard to the breakpoint, there will be further selection for amplification by the pair of the second round primers which bound the breakpoint. Without limiting the present invention in any way, the second round of PCR amplification provides additional specificity for amplification of the breakpoint region. Following the second round PCR, successful amplification of the sequence surrounding the breakpoint will be evident as a band of amplified material on electrophoresis.

Since it is not known precisely where the breakpoint lies, it is possible that one or more of the internal primers may not hybridise to their target region sequence due to this sequence having been effectively spliced out during the translocation event. However, in one embodiment, the forward and reverse primers selected for the first round amplification are directed to amplifying from the 5' and 3' end regions, respectively, of the gene fragments flanking the breakpoint. The second round primers are then directed to internal regions of the gene fragments flanking the breakpoint, that is, the regions which are closer to the breakpoint than the regions targeted by the first round primers. Again, it would be appreciated that since the precise location of the breakpoint is not known, one or more of these forward and/or reverse primers may not hybridise to the DNA sample due to their target region sequence having been spliced out. In terms of the second round "internal primers", it should be understood that this is a reference to a population of primers of which at least one primer, but preferably all the primers, are designed to amplify the subject DNA from a point which, when considered in the context of the translocated gene itself (rather than the antisense strand or the amplification product), is 3' of the most 3' of the forward primers used in the first round amplification and 5' of the most 5' of the reverse primers used in the first round amplification. By using the approach of a two step amplification using

progressively more internally localised primers, amplification of DNA spanning the breakpoint region can be achieved without the requirement to perform long PCRs or to generate very long and cumbersome amplification products.

Reference to a "primer" or an "oligonucleotide primer" should be understood as a reference to any molecule comprising a sequence of nucleotides, or functional derivatives or analogues thereof, the function of which includes hybridisation to a region of a nucleic acid molecule of interest (the DNA of interest also being referred to as a "target DNA") and the amplification of the DNA sequence 5' to that region. It should be understood that the primer may comprise non-nucleic acid components. For example, the primer may also comprise a non-nucleic acid tag such as a fluorescent or enzymatic tag or some other non-nucleic acid component which facilitates the use of the molecule as a probe or which otherwise facilitates its detection or immobilisation. The primer may also comprise additional nucleic acid components, such as the oligonucleotide tag which is discussed in more detail hereinafter. In another example, the primer may be a protein nucleic acid which comprises a peptide backbone exhibiting nucleic acid side chains. preferably, said oligonucleotide primer is a DNA primer.

Reference to "forward primer" should be understood as a reference to a primer which amplifies the target DNA in the DNA sample of interest by hybridising to the antisense strand of the target DNA.

Reference to "reverse primer" should be understood as a reference to a primer which amplifies the target DNA in the DNA sample of interest and in the PCR by hybridising to the sense strand of the target DNA.

The design and synthesis of primers suitable for use in the present invention would be well known to those of skill in the art. In one embodiment, the subject primer is 4 to 60 nucleotides in length, in another embodiment 10 to 50 in length, in yet another embodiment 15 to 45 in length, in still another embodiment 20 to 40 in length, in yet another embodiment 25 to 35 in length. In yet still another embodiment, primer is about 26, 27, 28, 29, 30, 31, 32, 33 or 34 nucleotides in length. Without limiting the invention in any way, the primers are designed in one embodiment to have a  $T_m$  of 65 to 70°C. This enables the PCR to use a high annealing temperature, which minimises non-specific annealing and amplification. Each forward or reverse primer for the second round PCR is designed to hybridise to a sequence which is close, either downstream for the forward primer or upstream for the reverse primer, to the hybridisation sequence for its corresponding forward or reverse first-round primer. Designing the corresponding primers to hybridise to closely adjoining sequences minimises the probability that the translocation breakpoint will involve or occur between the hybridisation sequences. even if this does occur, the sequence surrounding the translation breakpoint can still be amplified by the immediately upstream or downstream, as the case may be, primer pair.

In the exemplified embodiment described herein, primers were chosen so that their binding sites were staggered with the separation between adjacent binding sites being approximately 500 bases. This was done so that the amplified material would have range in size, up to a maximum length of approximately 1 kilobase. This strategy is in contrast to the strategy of "Long PCR" which would require fewer primers and a less complex multiplex PCR reaction. The advantages of the strategy of the present invention are that the standard shorter PCR reaction is more robust and the amplified product can be sequenced immediately rather than requiring another

## 15

set of PCR reactions to break it up into smaller amplicons which are suitable for sequencing.

In terms of the number of primers which are used in the method of the invention, this can be determined by the person of skill in the art. With regard to the total number of primers, the variables which require consideration are the size of the gene region which is being targeted and the distance between the sequences to which the primers hybridise. In order to amplify PCR fragments which are no larger than about 1 kb, the primers can be designed to hybridise at intervals of approximately 500 bases. With regard to CML, nearly all BCR translocations involve one of two regions, each of approximately 3 kb in length. In this case, 12 outer forward primers and 12 corresponding inner primers may be used. The ABL gene, however, is larger, approximately 140 kb in length, and up to 280 outer reverse primers and 280 inner reverse primers may be used. In one particular embodiment, a combination of 6 forward primers and 24 reverse primers is used and in another embodiment a combination of 6 forward primers and 140 reverse primers. The primer number which is selected to be used will depend on the genes involved in the translocation and thus may vary from translocation to translocation and will involve consideration of the competing issues of the number of PCR reactions which are required to be performed versus the probability of generating non-specific products during a PCR reaction. As would be understood by the person of skill in the art, a large number of primers in each individual PCR reaction decreases the number of PCR reactions but increases the probability of non-specific amplification reactions.

In one embodiment, the method of the present invention is performed using at least three primers, in another embodiment at least four primers. In yet another embodiment said invention is performed using 6-10 primers, 6-15 primers, 6-20 primers, 6-25 primers or 6-30 primers. In still another embodiment there is used 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30 primers.

There is therefore preferably provided a method of identifying a gene breakpoint, said method comprising:

(i) contacting a DNA sample with

(a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

(b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;

(ii) amplifying the DNA sample of step (i);

(iii) optionally contacting the amplicon generated in step (ii) with:

(a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and

## 16

(b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

(iv) amplifying the DNA sample of step (iii);

(v) analysing said amplified DNA.

preferably, said gene breakpoint is a gene translocation breakpoint and still more preferably a chromosomal gene translocation breakpoint.

The primers which are used in the method of the present invention are of a relatively low individual concentration due to the starting primer pool comprising multiple individual primers. This reduces the risk of inducing inhibition of PCR.

In order to facilitate a successful amplification result, it is therefore necessary to enable the generation of sufficient amplicons for detection and isolation. In one aspect of the present invention, this can be facilitated by tagging the primers with an oligonucleotide which can be used as a primer hybridisation site. In addition to the primers directed towards genes A and B, each PCR reaction may therefore also contain concentrations of two oligonucleotides which are directed to the tag, as a primer hybridisation site. These oligonucleotide sequences act as primers and enable efficient secondary amplification of the amplicons generated by the initial hybridisation and extension of the primers directed towards genes A and B. In one embodiment, the primer which is directed to the tag exhibits a  $T_m$  of 65° C.-70° C. in order to minimise non-specific amplification. Thus these primers are

directed towards overcoming the potential problem posed by the low concentrations of the primers directed towards A and B. Nevertheless, in some situations it may not be necessary to use one or both tag primers. For example, when there are only six forward primers for the BCR gene each primer may be at a concentration which is sufficient for relatively efficient amplification. Still further, it should be appreciated that the oligonucleotide tags provide an additional use when they are present in the final PCR round, since the tag primers can also be used for sequencing. Accordingly, although the tag is suitable for use as a site for primer hybridisation, it should be understood that the subject tag may also be useful for other purposes, such as a probe binding site in the context of Southern gel analysis or to enable isolation of the primer or the amplicon extended therefrom. To this end, the tag may com-

prise a non-nucleic acid component, such as a protein molecule or biotin which would enable isolation, for example by affinity chromatography, streptavidin binding or visualisation.

In order to ensure that these tags do not interfere with the extension of the primer, the primers are linked to the oligonucleotide tag at their 5' end. Reference to "oligonucleotide tag" should therefore be understood as a reference to a nucleotide sequence of less than 50 nucleotides which is linked to the 5' end of the forward and reverse primers of the present invention. In one embodiment, the tag is 25-30 bases in length. It should also be understood that consistently with the definitions provided in relation to the forward and reverse

primers, the oligonucleotide tags herein described may also comprise non-nucleic acid components such as isolation or visualisation tags eg. biotin, enzymatic labels, fluorescent labels and the like. This enables quick and simple isolation or visualisation of the tagged primers or amplicons via non-molecular methods.

That the oligonucleotide tag is "operably linked" to the primer should be understood as a reference to those regions being linked such that the functional objectives of the tagged primer, as detailed hereinbefore, can be achieved. In terms of the means by which these regions are linked and, further, the means by which the subject oligonucleotide primer binds to its target DNA region, these correspond to various types of interactions. In this regard, reference to "interaction" should be understood as a reference to any form of interaction such as hybridisation between complementary nucleotide base pairs or some other form of interaction such as the formation of bonds between any nucleic or non-nucleic acid portion of the primer molecule or tag molecule with any other nucleic acid or non-nucleic acid molecule, such as the target molecule, a visualisation means, an isolation means or the like. This type of interaction may occur via the formation of bonds such as, but not limited to, covalent bonds, hydrogen bonds, van der Wals forces or any other mechanism of interaction. preferably, to the extent that the interaction occurs between the primer and a region of the target DNA, said interaction is hybridisation between complementary nucleotide base pairs. In order to facilitate this interaction, it is preferable that the target DNA is rendered partially or fully single stranded for a time and under conditions sufficient for hybridisation with the primer to occur.

Without limiting the present invention to any one theory or mode of action, the inclusion of an oligonucleotide tag which can itself function as a primer hybridisation site can assist in facilitating the convenient and specific amplification of the amplicon generated by the forward and reverse primers of the present invention. Accordingly, this overcomes somewhat the amplification limitation which is inherent where a relatively low starting concentration of the forward and reverse primers is used. Where the starting concentration of forward and reverse primers is sufficiently high, it may not be necessary to use a tag. Accordingly, in a preferred embodiment, the DNA sample of interest is contacted with both the forward and reverse primers of the present invention and primers directed to the oligonucleotide tags of the forward and reverse primers such that the amplification reaction of step (ii) proceeds in the context of all these primers. It should be understood, however, that although it is preferred that amplification based on both the gene primers and the tag primers is performed simultaneously, the method can be adapted to perform the tag primer based amplification step after the completion of the gene primer based amplification.

The DNA sequence of the tags may be the same or different. With respect to a first round amplification, the tags may be the same if the purpose is to amplify the initial amplification product. However, if one wishes to selectively enrich for amplicons containing the sequence of one of the flanking genes, the primer directed to the tag region of the primer of the gene of interest (eg. gene A) should differ to the primer directed to the tag region of the primer of the other gene (eg. gene B). In another example, in terms of a second or subsequent round of amplification, the tags which are used for sequencing would be required to be different to prevent the simultaneous sequencing of both strands.

The present invention therefore provides a method of identifying a gene translocation breakpoint, said method comprising:

- (i) contacting a DNA sample with:
    - (a) one to thirty forward primers directed to a DNA region of the antisense strand of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
    - (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' relative to the gene breakpoint, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;

    - (c) a primer directed to the forward primer oligonucleotide tag of step (i)(a); and
    - (d) a primer directed to the reverse primer oligonucleotide tag of step (i)(b);
  - (ii) amplifying the DNA sample of step (i);
  - (iii) optionally contacting the amplicon generated in step (ii) with:
    - (a) one to thirty forward primers directed to a DNA region of the flanking gene or fragment thereof located 5' relative to the gene breakpoint, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
    - (b) twenty-four to four hundred reverse primers directed to a DNA region of the flanking gene or fragment thereof located 3' to the gene breakpoint, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
    - (c) a primer directed to the forward primer oligonucleotide tag of step (iii)(a); and
    - (d) a primer directed to the reverse primer oligonucleotide tag of step (iii)(b);

wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);

    - (iv) amplifying the DNA sample of step (iii);
    - (v) analysing said amplified DNA.
  - preferably said gene translocation breakpoint is a chromosomal gene translocation breakpoint.
- It should be understood that the oligonucleotide primers and tags of the present invention should not be limited to the specific structure exemplified herein (being a linear, single-stranded molecule) but may extend to any suitable structural configuration which achieves the functional objectives detailed herein. For example, it may be desirable that all or part of the oligonucleotide is double stranded, comprises a looped region (such as a hairpin bend) or takes the form of an open circle confirmation, that is, where the nucleotide primer is substantially circular in shape but its terminal regions do not connect.

19

Facilitating the interaction of the nucleic acid primer with the target DNA may be performed by any suitable method. Those methods will be known to those skilled in the art.

Methods for achieving primer directed amplification are also very well known to those of skill in the art. In a preferred method, said amplification is polymerase chain reaction, NASBA or strand displacement amplification. Most preferably, said amplification is polymerase chain reaction. To this end, in one embodiment of the invention, a 20 minute hybridisation provides good amplification in the first round PCR.

Reference to a "sample" should be understood as a reference to either a biological or a non-biological sample. Examples of non-biological samples includes, for example, the nucleic acid products of synthetically produced nucleic acid populations. Reference to a "biological sample" should be understood as a reference to any sample of biological material derived from an animal, plant or microorganism (including cultures of microorganisms) such as, but not limited to, cellular material, blood, mucus, faeces, urine, tissue biopsy specimens, fluid which has been introduced into the body of an animal and subsequently removed (such as, for example, the saline solution extracted from the lung following lung lavage or the solution retrieved from an enema wash), plant material or plant propagation material such as seeds or flowers of a microorganism colony. The biological sample which is tested according to the method of the present invention may be tested directly or may require some form of treatment prior to testing. For example, a biopsy sample may require homogenisation prior to testing or it may require sectioning for in situ testing. Further, to the extent that the biological sample is not in liquid form, (if such form is required for testing) it may require the addition of a reagent, such as a buffer, to mobilise the sample.

To the extent that the target DNA is present in a biological sample, the biological sample may be directly tested or else all or some of the nucleic acid material present in the biological sample may be isolated prior to testing. It is within the scope of the present invention for the target nucleic acid molecule to be pre-treated prior to testing, for example inactivation of live virus or being run on a gel. It should also be understood that the biological sample may be freshly harvested or it may have been stored (for example by freezing) prior to testing or otherwise treated prior to testing (such as by undergoing culturing).

Reference to "contacting" the sample with the primer should be understood as a reference to facilitating the mixing of the primer with the sample such that interaction (for example, hybridisation) can occur. Means of achieving this objective would be well known to those of skill in the art.

The choice of what type of sample is most suitable for testing in accordance with the method disclosed herein will be dependent on the nature of the situation, such as the nature of the condition being monitored. For example, in a preferred embodiment a neoplastic condition is the subject of analysis. If the neoplastic condition is a lymphoid leukemia, a blood sample, lymph fluid sample or bone marrow aspirate would likely provide a suitable testing sample. Where the neoplastic condition is a lymphoma, a lymph node biopsy or a blood or marrow sample would likely provide a suitable source of tissue for testing. Consideration would also be required as to whether one is monitoring the original source of the neoplastic cells or whether the presence of metastases or other forms of spreading of the neoplasia from the point of origin is to be monitored. In this regard, it may be desirable to harvest and test a number of different samples from any one mammal.

20

Choosing an appropriate sample for any given detection scenario would fall within the skills of the person of ordinary skill in the art.

The term "mammal" to the extent that it is used herein includes humans, primates, livestock animals (e.g. horses, cattle, sheep, pigs, donkeys), laboratory test animals (e.g. mice, rats, rabbits, guinea pigs), companion animals (e.g. dogs, cats) and captive wild animals (e.g. kangaroos, deer, foxes). preferably, the mammal is a human or a laboratory test animal. Even more preferably the mammal is a human.

As detailed hereinbefore, in one embodiment the method of the present invention is performed as a sequential two step amplification using multiple second round primers each of which is directed to a gene region which is either 3' (for the forward primers) or 5' (for the reverse primers) to that which is targeted by the corresponding first round primers. The person of skill in the art would appreciate that in some cases it may not be necessary to conduct a second round amplification. The necessity to perform a second round amplification may also be obviated if a selective or enrichment step as described below is performed. This situation may arise when the sequence around the breakpoint is amplified very efficiently and there is very little non-specific amplification such that a clearly defined band of amplification product is observed on electrophoresis of the product of the first round amplification or if the subsequent selection step is very efficient. In general, however, it is expected that a sequential two step amplification process would be used in order to minimise non-specific amplification and to generate a relatively short amplification product which spans the breakpoint region. In general, it is expected that the amplification product would be less than 1.5 kb, less than 1 kb, less than 0.8 kb or less than 0.5 kb. It should be understood that depending on the size of the genes which have been translocated, the method of the invention may be adapted to incorporate third or fourth round amplification steps in order to further minimise non-specific amplification. This can be an issue owing to the number of primers present in the multiplexed reaction and to the fact that one of the genes participating in the translocation often contains multiple repetitive sequences such as Alu. Nevertheless, it is expected that the need for further rounds of amplification would be unlikely.

Although the method of the present invention has been designed such that the amplification steps can be sequentially performed directly on the amplification product of a previous amplification, this should not be understood as a limitation in terms of whether any additional steps are sought to be incorporated by the skilled person, such as enrichment/selection steps. For example, one may seek to select for the desired amplicons after the first round amplification and to thereafter conduct the second round amplification on their material alone. Methods which one could utilise to select or enrich include:

(i) a selection step based on the unique oligonucleotide tags which are linked to the primers. Accordingly, since the tags themselves are also amplified and therefore form part of the amplicon, they could be used as a probe site to enable isolation of amplicons which are the result of both forward and reverse primer amplification and therefore should span the breakpoint. Alternatively, biotinylation of one of the tags provides means of identifying and isolating amplicons which have resulted from extension by either the forward or reverse primers. For example, by flooding the amplification product with biotinylated primer, the primer can act as a probe to identify the amplicons of interest and the biotinylation can provide a basis for isolating those amplicons. By ensuring that each of the primer groups of the

present invention comprises a unique tag, it is possible to select out, with significant particularity, only specific amplicons of interest. In particular, the skilled person would seek to exclude amplicons which have been amplified by a forward primer but which have not then been amplified by a reverse primer, thereby indicating that the subject amplicon possibly does not extend across the breakpoint. By selecting out the amplicons which are most likely spanning the breakpoint, a subsequent round of amplification is more specifically targeted and less likely to generate unwanted amplicons as a result of either inherent cross-hybridisation of primers or the amplification of amplicons which do not flank both sides of the breakpoint.

- (ii) One may seek to run the products on a gel and excise out only certain bands or regions which are likely to be relevant and thereafter subject these to a further amplification step. When a band is present on the gel after the second round amplification, if there are any problems in sequencing an attempt can be made to clean it up by cutting the product out of the gel and performing a series of PCR reactions using individual primers and/or smaller pools of primers. For example, one might use individual forward BCR primers and pools containing only 12 reverse ABL primers.
- (iii) one may expose the amplified products to one or more rounds of bottleneck PCR in order to provide negative selection against non-specific amplified products.

Without limiting the application of the present invention to any one theory or mode of action, in a classical PCR, the primers and reaction conditions are designed so that primer hybridisation and extension of the forward and reverse primers occur at or close to the maximum efficiency so that the number of amplicons approximately doubles with each cycle resulting in efficient exponential amplification. Bottleneck PCR, however, is predicated on the use of forward and reverse primer sets where the primers of one set have been designed or are otherwise used under conditions wherein they do not hybridise and extend efficiently. Accordingly, although the efficient primer set will amplify normally, the inefficient set will not. As a consequence, when a sequence of interest is amplified, the number of amplicon strands is significantly less than that which would occur in a classical PCR. Efficient amplification only commences once amplicons have been generated which incorporate, at one end, the tag region of the inefficient primer. At this point, the primers directed to the tag regions effect a normal amplification rate. A "bottleneck" is therefore effectively created in terms of the generation of transcripts from the inefficient primer set.

A more severe bottleneck is usefully created where the inefficient primers are directed to commonly repeated sequences, such as an alu sequence. Amplification of unwanted product may result if such binding sites are closely apposed and if the inefficient primers can act as forward primers and reverse primers. However, owing to both primers being inefficient, amplification is initially extremely inefficient and there is a severe bottleneck. Efficient amplification only commences once amplicon strands have been generated which comprise the tag region of the inefficient primer at one end and its complement at the other. After any given number of cycles, the number of such amplicons is, however, substantially less than that which occurs during amplification of the sequence of interest. The amount of unwanted product at the end of the amplification reaction is correspondingly reduced.

Hybridisation and extension of an inefficient primer which has correctly hybridised to the sequence of interest followed in a subsequent cycle by hybridisation and extension of an efficient primer to the previously synthesised amplicon generates a template to which the tag primer can efficiently

hybridise and extend. Since such molecules together with their complements provide upstream and downstream binding sites, each for an efficient primer (the tag primer and one member of the efficient set), succeeding cycles of amplification from such templates are both efficient and exponential. The result is that, after an initial lag or "bottleneck", the overall rate of amplification speeds up in later cycles so that a near doubling of amplicon number with each cycle results. However, the net result is that there is negative selection against amplification of undesired amplicons as compared to amplicons of the sequence of interest, owing to the bottleneck at each end for the former and only at one end for the latter.

Accordingly, if the same number of commencing target sequences is considered and comparison to the amplification produced by classical PCR is made, application of the bottleneck PCR will produce a lesser increase in the number of amplicons of the sequence of interest and an even lesser increase in the number of amplicons of unwanted sequences. Although amplification of both wanted and unwanted products occurs, there is relative enrichment of the sequence of interest relative to the unwanted sequences. There is an inverse relationship between absolute amplification and enrichment since decreasing the efficiency of the inefficient primer set produces increased enrichment at the expense of lesser amplification.

Once the amplification rounds have been completed, the amplicons spanning the breakpoint region can be analysed. In a preferred embodiment, the subject amplicon is isolated by excision of a gel band containing that amplicon and sequenced in order to characterise the breakpoint region. To the extent that a band excised from a gel is to be analysed, it may be necessary to further amplify the DNA contained therein in order to provide sufficient material for sequencing. The oligonucleotide tags hereinbefore described provide a suitable primer hybridisation site to facilitate further amplification of the isolated amplicons.

As detailed hereinbefore, the method of the present invention provides a simple and routine means of identifying and characterising any breakpoint region, such as the nature, accuracy and stability of a site directed insertion of a gene into a chromosome or vector (this being important in the context of gene therapy), but in particular the chromosomal gene translocation breakpoints that are characteristic of many diseases. Examples of such translocations and diseases include, but are not limited to:

- t(2;5)(p23;q35)—anaplastic large cell lymphoma
- t(8;14)—Burkitt's lymphoma (c-myc)
- t(9;22)(q34;q11)—Philadelphia chromosome, CML, ALL (BCR-ABL recombination)
- t(11;14)—Mantle cell lymphoma (Bcl-1)
- t(11;22)(q24;p11.2-12)—Ewing's sarcoma
- t(14;18)(q32;p21)—follicular lymphoma (Bcl-2)
- t(17;22)—dermatofibrosarcoma protuberans
- t(15;17)—acute promyelocytic leukemia (pml and retinoic acid receptor genes)
- t(1;12)(q21;p13)—acute myelogenous leukemia
- t(9;12)(p24;p13)—CML, ALL (TEL-JAK2)
- t(X;18)(p11.2;q11.2)—Synovial sarcoma
- t(1;11)(q42.1;q14.3)—Schizophrenia
- t(1;19)—acute pre-B cell leukemia (PBX-1 and E2A genes).

preferably, said chromosomal gene translocation is a BCR-ABL translocation or a PML-RARalpha translocation.

According to this preferred embodiment there is provided a method of identifying a chromosomal BCR-ABL translocation breakpoint, said method comprising:

## 23

- (i) contacting a DNA sample with:
  - (a) one or more forward primers directed to a DNA region of BCR or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to a DNA region of ABL or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (ii) amplifying the DNA sample of step (i);
- (iii) optionally contacting the amplicon generated in step (ii) with:
  - (a) one or more forward primers directed to a DNA region of BCR or fragment thereof, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag; and
  - (b) one or more reverse primers directed to ABL or fragment thereof, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) analysing said amplified DNA.

preferably, said amplification steps are performed using 1-30 forward primers and 24-300 reverse primers.

In terms of the embodiment of the invention exemplified herein, primers were chosen so that their binding sites were staggered with the separation between adjacent binding sites being approximately 500 bases. This was done so that the amplified material would have range in size, up to a maximum length of approximately 1 kilobase. This strategy may be contrasted to the prior art strategy of "Long PCR" which would require fewer primers and a less complex multiplex PCR reaction. One of the advantages of the strategy of the present invention is that the standard shorter PCR reaction is more robust and the amplified product can be sequenced immediately rather than requiring another set of PCR reactions to break it up into smaller amplicons which are suitable for sequencing.

The present invention therefore preferably provides a method of identifying a chromosomal BCR-ABL translocation breakpoint, said method comprising:

- (i) contacting a DNA sample with:
  - (a) one to thirty forward primers directed to a DNA region of BCR or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) twenty-four to four hundred reverse primers directed to a DNA region of ABL or fragment thereof, which primers are optionally operably linked at their 5' end to an oligonucleotide tag;

## 24

- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags;
- (c) a primer directed to the forward primer oligonucleotide tag of step (i)(a); and
- (d) a primer directed to the reverse primer oligonucleotide tag of step (i)(b);
- (ii) amplifying the DNA sample of step (i);
- (iii) contacting the amplicon generated in step (ii) with:
  - (a) one to thirty forward primers directed to a DNA region of BCR or fragment thereof, which primers are directed to DNA regions which are located 3' to one or more of the forward primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (b) twenty-four to four hundred reverse primers directed to a DNA region of ABL or fragment thereof, which primers are directed to DNA regions which are located 5' to one or more of the reverse primers of step (i) and which primers are optionally operably linked at their 5' end to an oligonucleotide tag;
  - (c) a primer directed to the forward primer oligonucleotide tag of step (iii)(a); and
  - (d) a primer directed to the reverse primer oligonucleotide tag of step (iii)(b);
- wherein the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a) and the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(a) but which forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i);
- (iv) amplifying the DNA sample of step (iii);
- (v) isolating and sequencing said amplified DNA.

More preferably, said DNA sequence is a blood derived sample.

The method of the present invention has broad application including, but not limited to:

- (i) enabling the design and generation of patient specific probes which can be used for the ongoing monitoring of a patient who is diagnosed with a disease condition characterised by chromosomal gene translocation. Results obtained by this means for chronic myeloid leukemia are shown in FIG. 6.
- (ii) the analysis and monitoring of in vitro and in vivo gene transfection systems which are directed to integrating a gene or other DNA region into a chromosome, vector, plasmid, artificial chromosome or the like. Where the general site at which recombination should occur is known, the present invention can be applied to determine the specific point and nature of the integration (i.e. the breakpoint). It can also be used to monitor the ongoing stability of the genetic recombination event by virtue of enabling the generation of specific primers.

Accordingly, in yet another aspect there is provided a method of monitoring a disease condition in a mammal, which disease condition is characterised by a gene breakpoint, said method comprising screening for the presence of said breakpoint in a biological sample derived from said mammal, which breakpoint has been identified in accordance with the method hereinbefore defined.

Methods of screening for the subject breakpoint would be well known to those skilled in the art and include any suitable

**25**

probe-based screening technique, such as PCR based methods. By virtue of the identification of the breakpoint region in accordance with the method of the invention, one can design an appropriate probe set to specifically amplify the subject breakpoint.

In one embodiment, said gene breakpoint is a chromosomal gene translocation breakpoint such as:

t(2;5)(p23;q35)  
t(8;14)  
t(9;22)(q34;q11)  
t(11;14)  
t(11;22)(q24;q11.2-12)  
t(14;18)(q32;q21)  
t(17;22)  
t(15;17)  
t(1;12)(q21;p3)  
t(9;12)(p24;p13)  
t(X;18)(p11.2;q11.2)  
t(1;11)(q42.1;q14.3)  
t(1;19).

In another embodiment, said condition is:

anaplastic large cell lymphoma  
Burkitt's lymphoma  
CML, ALL  
Mantle cell lymphoma  
Ewing's sarcoma  
follicular lymphoma  
dermatofibrosarcoma protuberans  
acute promyelocytic leukemia  
acute myelogenous leukemia  
Synovial sarcoma  
Schizophrenia; or  
acute pre-B cell leukemia.

Still another aspect of the present invention is directed to a DNA primer set, which primer set is designed to amplify and/or otherwise detect a gene breakpoint, which breakpoint has been identified in accordance with the method hereinbefore defined.

The present invention is now described by reference to the following non-limiting examples and figures.

#### Example 1

##### Isolation of BCR/ABL Breakpoint Product from gDNA of Patient 1

Genomic DNA extracted by Qiagen Flexigene kit  
1<sup>st</sup> Round PCR (50 ng genomic DNA)—all reactions performed in duplicate

Forward primer pool—FA (Contains 7 forward BCR primers BCRF1-BCRF7 each with same 5' tag sequence (A), Total 50 ng (7.14 ng each)

Reverse primer pool—R3/4 (Pool of 24 oligonucleotide reverse ABL primers, each with same 5' tag sequence (C), Total 50 ng (2.08 ng each)

Forward and reverse tag sequence primers (A,C)—25 ng of each

PCR Conditions

1×PCR buffer, 5 mM MgCl<sub>2</sub>, 0.75 ul dUTP (300 uM each), 0.4 ul Platinum Taq (2 U)

Cycling Conditions

95/4 min (97° C./1 min, 65° C./20 min, 72° C./1 min)×5

(96° C./30 sec, 65° C./20 min, 72° C./1 min)×5

(92° C./30 sec, 65° C./20 min, 72° C./1 min)×10

2<sup>nd</sup> Round PCR (1<sup>st</sup> round reaction diluted 1/200 in sterile water)

**26**

Forward primer pool—NFA (Contains 7 forward internal BCR primers BFN1-BFN7 each with same 5' tag sequence (B), Total 50 ng (7.14 ng each)

Reverse primer pool—RN3/4 (Pool of 24 oligonucleotide reverse internal ABL primers, each with same 5' tag sequence (D), Total 50 ng (2.08 ng each)

Forward and reverse tags (B,D)-25 ng of each

PCR Conditions

10 1×PCR buffer, 5 mM MgCl<sub>2</sub>, 0.75 ul dUTP (300 uM), 0.4 ul Pt Taq (2 U)

Cycling Conditions

95/4 min

(94° C./30 sec, 65° C./10 min, 72° C./1 min)×10

15 (94° C./30 sec, 65° C./5 min, 72° C./1 min)×15

PCR products (7 ul) resolved on 1.5% (v/v) agarose gel at 120 volts

Identification of BCR/ABL Breakpoint from Patient 1

20 PCR products resolved on 1.5% (v/v) agarose gel at 120 volt

Band excised and purified via Flexigene kit

Reamplification of bands by PCR (1/1000 dilution of purified product)

25 Forward primer—Tag B (25 ng)

Reverse primer—TagD (25 ng)

PCR Conditions

1×PCR buffer, 5 mM MgCl<sub>2</sub>, 0.75 ul dUTP (300 uM), 0.4 ul Pt Taq (2 U)

30 Cycling Conditions

95/4 min

(94° C./30 sec, 65° C./30 sec, 72° C./30 sec)×35

PCR Product Sequenced with TagB Primer (Flinders Sequencing Facility)

Confirmation of Breakpoint by PCR

PCR performed on gDNA (50 ng) across breakpoint

Patient 1 gDNA vs 10× Normal gDNA (several primer combinations)

40 Forward primer—BCR (patient specific) (25 ng)

Reverse primer—ABL (patient specific) (25 ng)

PCR Conditions

1×PCR buffer, 5 mM MgCl<sub>2</sub>, 0.75 ul dUTP (300 uM), 0.4 ul Pt Taq (2 U)

45 Cycling Conditions

95/4 min

(97° C./1 min, 65° C./30 sec, 72° C./30 sec)×5

(96° C./30 sec, 65° C./30 sec, 72° C./30 sec)×5

(92° C./30 sec, 65° C./30 sec, 72° C./30 sec)×25

PCR products resolved on 3% (v/v) agarose gel at 120 volt  
Band excised and purified via Qiagen minElute kit

55 Products sequenced with 5' BCR specific primer to confirm BCR/ABL breakpoint (Flinders sequencing facility).

Nearly all translocations involve a 3 kb region of the BCR gene and 140 kb region of the ABL gene. Six forward primers used to cover the region of the BCR gene and 282 primers used to cover the region of the ABL gene. Six PCRs are set up, each containing one of the BCR primers, all of the ABL primers, and the common tag primer.

If necessary, a second round of PCR is performed with a nested internal BCR primer and 282 nested internal ABL primers Alternatively, 1-3 rounds of Bottleneck PCR are performed in order to remove non-specific amplified products and reveal the amplified translocation sequence.

**27**

The ABL gene is very rich in Alu sequences, and the BCR gene also contains one such sequence. The ABL primers have therefore undergone a selection procedure which sequentially involves, for each ABL primer:

design using standard criteria

5

pairing with each BCR primer and testing by electronic

PCR for amplification off the BCR template. Primers that fail this criterion are discarded.

incorporation in a pool of 12 or 24 ABL primers, pairing the pool with each BCR primer, and testing by experimental PCR using a BCR template which has been previously produced by PCR amplification. Any pool that that produces amplification and thus fails this test is further analysed by testing each of the individual ABL primers to determine which is responsible for amplification. When identified, this primer is discarded.

The BCR and ABL primers used in Example 1 are shown in Example 2.

**Example 2**

20

Primers Used for Isolation of BCR-ABL Translocation Breakpoint in Chronic Myeloid Leukemia

25

**BCR Primers****1st Rd**

BCRF1 -FT0 ctttccctgacatccgtgg

30

BCRF2 -FT0 (-5) acacagcatacgcstatgcacatgtg

R15

BCRF3 -FT0 gaggttgttcagatgaccacgg

R16

BCRF4 -FT1 (-10) cagctactggagctgtcagaacag

35

BCRF5 -FT0 tgggcctccctgcattcc

R17

BCRF6 -FT0 tccccctgcacccacgg

R18

**2nd Rd**

BCRF1 -FT1 tgacatccgtggagctgcagatgc

40

BCRF2 -FT1 acatgtgtccacacacacccacc

R21

BCRF3 -FT1 accacgggacaccccttgaccctgg

R22

BCRF4 -FT1 (-4) ctggagctgtcagaacagtgaagg

45

BCRF5 -FT1 tccctgcattccctgcattccctcc

R25

BCRF6 -FT1 cccacgacttccagcactgagc

R26

The second round primers were internal to the first round primers and were used either for a second round together with internal ABL primers or for performing Bottleneck PCR in order to eliminate non-specific amplified material and facilitate isolation of the translocation breakpoint.

Various combinations of the forward and reverse primers can be used. In one embodiment, the protocol that was used was to set up 6 PCRs, each containing a different BCR primer and all 282 ABL primers

282 Reverse ABL Primers Used for the First PCR Round and the Tag Sequence which was on the 5' End of Each Primer

50

R27

R28

R29

R30

R31

R32

R33

R34

R35

R36

R37

R38

R39

R40

R41

R42

**28****-continued**

R3 cactcctgcactccagcctgg

R4 caaccaccaaagtgtttctctgg

R5 atatggcatctgttaatattaccacc

R6 tgcctcggecccccggaaagtgc

R7 agccaccacacccagccagg

R8 aataactgtttctccccccaaaac

R9 tggggatcaaaaaatggggccatacc

R10 acttaagcaatttttccataaaaagg

R11 ctttcaattgtgttaccaactctcc

R12 acctcctgcattctccctttgc

R13 aaataaaagtttggaaaccataagtgg

R14 caccatcacagctactgcagc

R15 aacctcttgagaatcggttagcc

R16 aaataaaagtcataccctcaattttgc

R17 gacacattccatgggttaattcc

R18 tggaaaatatgggttcaagggagg

R19 gcaggtggataacgaggtcagg

R20 ccagccaagaatttcaaaggataggc

R21 gaaggggatgacaaaggaaacg

R22 gcagaagaactgcttgcacccctgg

R23 gtggcccttgcactcgagagg

R24 ccctcagaaaaactactgaaaagg

R25 tagaaaccaagatatctagaattccc

R26 ccacggccggcgaaataatgc

R27 aaaaaaaaaaggggaaaaactgagag

R28 ctgggcgcagtggctcatgcc

R29 tggctgtgaggctgagaactgc

R30 ctgggcgcacagagtgagactcc

R31 aagtctggctggcgcagtgg

R32 aatggacaaaagggtgaactggc

R33 gatagagtgaaaacgcacaatggc

R34 aattaaacagcttaggtcaatatgagg

R35 ggtctccactatcaagggacaag

R36 aagcagctgttagtcattccagg

R37 aggcatcctcagattatggctcc

R38 cctgagtaacactgagaccctgc

R39 aacactcaagctgtcaagagacac

R40 attcaggccaggcgcaagtggc

R41 taaatcgtaaaaactgcccacaaaagc

R42 cagaggagtagggagaaggaaaagg

Tag A gcaacactgtgacgtactggagg

R1 gtctatctaaaattcacaaggatgc

R2 aggcaaagtaaaatccaaagcaccc

60

R43

R44

R45

R46

## US 9,145,587 B2

**29**

-Continued  
R43 ggtagcttatctaccaagtagaatcc  
R44 atcagattggaaaagtcccaaagc  
R45 ctccctgaaaaggcacctactcagc 5  
R46 ctccctaaacctgaggacttggg  
R47 ttttccttaatagaccaccattcc  
R48 ctgcgttattaccatcaactcatgtc 10  
R49 ctggccaacatagtgaaaccacg  
R50 atttgaatagggttaaaagtatccatg  
R51 cacttcagtggaaagtggcatgc 15  
R52 gttttcttcgaagtgataaacatacg  
R53 gctcccttagtctatgtacctgtgg  
R54 tactctggcatggtaactgggc 20  
R55 acaaaggactaggctgtggagc  
R56 ccaagttaccaaattaccaaagttacc  
R57 tgagccgatatacgcggactgc 25  
R58 tcccaataaaagggttgcccagg  
R59 ctgggttagcaaattagggaaacagg  
R60 ctggccagaaaagacagttttatcc 30  
R61 gtttccaggaaaggataacacc  
R62 tcactccaggaggttccattcc  
R63 aggcttggaaataagcagcagctgg  
R64 attcatacaatggataactactcagc 35  
R65 taagtgtatccctccacactcaacc  
R66 tataagaggaagactggggctgg  
R67 tcatacttatgcagggtttagggg 40  
R68 caagatcacgcactgcactcc  
R69 aaaataataagctgggtcaagatc  
R70 caccagcctcattcaacagatgg 45  
R71 caatgcagcctcaacctctgg  
R72 gtttaggtcagggtctatgtctg  
R73 aagtttcaaaaggacatgtacaaaatg 50  
R74 tcctgaagaggctgcagttcc  
R75 ctgggtcacatcccaaggctgtgc  
R76 catgtggccatgttcttgagg 55  
R77 ctcagcctcccgagttagtgg  
R78 aaagacattnaagaggagatgggc  
R79 tgctgggattacaggcgtgagc 60  
R80 tgtgacttccatccgcagctcc  
R81 gacacttttgtggagcttcatgg  
R82 catgtgagggggcacgttgc 65  
R83 tcttcctatgagaaaagtgggtgc

**30**

-continued  
R84 tggcaaaatgttatcgagctgcc  
R85 tatgaacacagccggcctcagg  
R86 gaggttgcagtgagctgagatcg  
R87 gtcaagcaccaggatccgatacc  
R88 atctgggtttgggtggcgcacg  
R89 gttaagcgggtcccacatcagc  
R90 cagccagtttcaagtagaaagatgc  
R91 gacccaaagcataagggactagc  
R92 cccaaaaagttacaagagaaatttc  
R93 cgcctgtatcccagctactcg  
R94 cgctgtatgcggaaaagaaatcc  
R95 tctactatgaaccctccttcagac  
R96 gtgtggatatacggtgtgagc  
R97 ttatccaaatgtcccaggcagg  
R98 ctgccagcactgctgccagc  
R99 gctactgcaggcagtgccccc  
R100 catccaagccaaagggtgtcagg  
R101 tgggtcatgtatccaggaaagcc  
R102 gatccgtcactgttaacactcagg  
R103 ctcacagtcaacaagctctgagc  
R104 gagatgtatgtgggtcacagg  
R105 ttagaagaatgggatcgcaaaagg  
R106 cggtattcaaatatgaggctaggc  
R107 gtaatccctgtccagtcctcc  
R108 acagggtcagacagagccttgg  
R109 agttattgtatctaactataacaacaagc  
R110 aaagacttagggccggggacg  
R111 ctggtagaaataaagacaacaagcc  
R112 gtgccaagtaattaaaagttgaaacc  
R113 ggctttgaaggaggcaccacc  
R114 gaaggataatacctatgataacttcc  
R115 ggcaggaaatactgtgcttcaag  
R116 gtggtaaaatccacctcagttacc  
R117 tcccaaaagtgtggattacagg  
R118 gaaatttagcaaacaatgccaagacg  
R119 taagtattggaccgggaaggagg  
R120 ctatcatggctcaaaagtgttagcc  
R121 atttcacaaactacagaggccagg  
R122 tagacttctgtctctatgtctgc  
R123 tgagttagtgcctatgtgatacc

## US 9,145,587 B2

**31**

R124	-Continued	
	acttcacaccaggctgtccacc	
R125	taactcatatcctcgagagagacc	
R126	agaggttcctcgatttccctgc	5
R127	gtgtcagcgtccaaacacaaagc	
R128	gaaagtggatggcaagcattgc	
R129	gtgatcacctcacagctgcagg	10
R130	gtttgttagtcaaggcatttacc	
R131	cctcagcctccagagtagctgg	
R132	taaaagaaaactcctccctcctgg	15
R133	aatgtgctatgtcttaatccatgg	
R134	agctggcaaattcgttatataaaag	
R135	gcttgaaccttggaaagggtggagg	20
R136	gcaggcatgctaagacaccttcagc	
R137	cagctccatgataactccacagg	
R138	gcttgaacccaggaggcgagg	25
R139	atcgaagatgccactgcaagagg	
R140	ccaaccacacttcaggggatacc	
R141	cacgcaggactccactgatactcac	30
R142	gggttccatgttggcagg	
R143	cccaacaaaggctctggcctgg	
R144	atgacagcagaggagcttcatcc	
R145	gcaggctacgagtaaaaggatgg	35
R146	cgggtaaaatcttgcccttc	
R147	aaacttaaacaatggatgtgg	
R148	agagactgaggaaactgttccagc	40
R149	gaaacggtcttggatcaactgatcc	
R150	tgcgcatacatcttgttccagg	
R151	ggcctccgtttaactgttgtc	45
R152	gaatgtggccgcacacagtgg	
R153	tcttggatagaaaaggcagctgg	
R154	gc当地agccaaagggccctgg	50
R155	ttctccaaaaatgagccccaaagg	
R156	gtggtagctaaacaaaaggatacc	
R157	gcaaaatccatgtgaatcttattggc	55
R158	cctgatctatggAACAGTGGTGG	
R159	gttacaaacgttgcagttgcacg	
R160	gaaccccgtcaacagtgtatcc	60
R161	acaggacactcaaggcaaggagc	
R162	catacctaaaatgaaaaatgtctatccc	
R163	gagttgcataatgtttataatccc	65
R164	tgagcccacatccataaagttagc	

**32**

R165	-continued	
	accgcaaccttgcgcctgg	
R166	taaatatTTGATGGAGTCACCAC	
R167	aaagccaggaaaaagttatgagg	
R168	tcccaaagtcccaggattacagg	
R169	tcaactatggagcatctccgatgg	
R170	agttcccttggaaagtctccgagg	
R171	aaaataatcacccagcccacatcc	
R172	acaaaactacagacacagaaaagtgg	
R173	tttgggaggctgaggttagtgg	
R174	aaagacagtgaaacatctataaggg	
R175	cattttggagaccaggcagg	
R176	gcatgggacagacacaaaggcagc	
R177	gaataacaaagagagccggctgg	
R178	taaacctttattgaaaattgtcaatgg	
R179	cgcctcagecctccaaagtgc	
R180	tacatttagtttataggtccagtagg	
R181	gaaggtttattcatattaaatgtgcc	
R182	ctggcttctgtggttgagttgg	
R183	acagacactacccataaggatgg	
R184	gctagttttgtgtgaaatgg	
R185	ggcctactcacacaatagaatacc	
R186	gcaccattgcactccagcctgg	
R187	gaaattaggataaaagggtgtcacagc	
R188	cagaagtgtcaagggtaaactgtc	
R189	ctgaatcatgaaatgttctactctgc	
R190	tgtcaacttgactggccatac	
R191	cctccgtatagttgggattatagg	
R192	gcttggagttcccttggaaattttgg	
R193	cctgggtggctccagtttctacc	
R194	aactcctgacactcatgatccacc	
R195	gctgggattacaggcatgagcc	
R196	ttctcccttatccttggtgacattc	
R197	tcccaaagtgtgggattacagg	
R198	gtcataagtgcaggaccatctgc	
R199	ctgtttcattgatttccagactggc	
R200	gcaatctcggtcaactgcaagc	
R201	gaagaagtgtactatcatgatctgg	
R202	ttcaccatgttggccaggctgg	
R203	catcaactgaaatgacaactgagc	
R204	gtccagcctggcgatagagc	

US 9,145,587 B2

**33**

R205 -Continued  
gaggaaagtcttgaagaggaacc

R206 ggtacactcaccagcagtttgc

R207 gagcaactgggtgaatacatatgg

R208 caatacctggcaccacatacacc

R209 gggactacaggcatgtgccacc

R210 cggtggctcacgcgttaatcc

R211 caactgttaaatctctatggaaacc

R212 gacaaaggattagaaaatgcaccc

R213 gggaaatgttctaaaactggatttgtgg

R214 aataataatagccaggtgtggtagc

R215 ctggAACACTCACACATTGCTGG

R216 ctgggtgacagagcgagactcc

R217 cccaaATCATCCCCGTGAAACATGC

R218 gaccctgcaatcccaacactgg

R219 ctctcaggcCTTCAAACtACACC

R220 cagggaaagggtcgctcagtg

R221 atctgcaaAGCAGCAGAGCAGG

R222 gtacccatgacagacaAGTTAGG

R223 ctatcccTAActgtCTCCTTGG

R224 ggatggTCTCGATCTCTGACC

R225 aggttagAGACCTCTCTAATGC

R226 agctgggattacaggTGCCTGC

R227 gctgaggcaggTTGGGGTGC

R228 acattaacgttcctaacttCTCC

R229 gtgctgcGATTACAGGTGTGAGC

R230 tatgacAGCAGTATTATACTATCACC

R231 ctggggacAAATCTGAACtGCC

R232 gtagctattgttatttccAAAAGAGG

R233 gcttgggACCCCAGGACAAGG

R234 CCTGGCCAACATGGGAATCC

R235 aattgcttgaacCTGGGGAGGTGG

R236 gcctaAGACCCAAAAGCTTATTGC

R237 catattaaAGGGCCATTCAATTGG

R238 ggatgtAACCGAGTGTATCACAGG

R239 ggaAGTTAGTCACATCTCTAGC

R240 gcacccACAGGACAACCAACCG

R241 gggacgcgcCTGTAAACAAAGG

R242 gggctggggccacgcTCC

R243 cgcaAAAGTGAAGCCCTCTGG

R244 gaaatcctACTTGATCTAAAGTGC

R245 tttgagcaacttggaaaaataAGCG

**34**

-continued

R246 ttccccAAAAGACAAATAGCACTTCC

R247 ccattttGAAAATCACAGTGAATTCC

R248 gaaaAGAAAACCCCTGAATTCAAAGG

R249 tgctgaaaAGAAGCATTAAAAGTGG

R250 ctcttAccAGTTAGCAGACTTCC

R251 ttttCAGCCAAAATCAAGGACAGG

R252 CTTGAGCCCAGGAGTTGAGACC

R253 CGCCTGTAGTACCCCTACTAGG

R254 ggtaaAGAAAGAAGGATTGAAAACC

R255 TAAGAGTAATGAGGTTAAAGTTATGC

R256 CATTTTATTGTCACAGGCCATTGC

R257 GCCACGCCCTCTCTGCCACC

R258 TGCCCTCCTGACTGCACTGTG

R259 CCATGCTTACCAACGCCCTGG

R260 CATTCAAGGCTGGAGTGCCTGG

R261 CTAAAAATTGTCGGCTAAGACATTG

R262 TTGCTTGTGCCCCGGTTGG

R263 GAGCTTAGAGGAAAAGTATTATTCC

R264 TGGTGTGTGCCAGACGCTGG

R265 CAGATCTTTGGCTATTGCTTGG

R266 GAAGGAAAGGGCCTCCACTGC

R267 CATGAAAAGCATGCTGGGGAGG

R268 CAAACATAAAAAGCTTAAAGAAGCC

R269 TCCCAACTATGAAAAATAGAAGACG

R270 CACAAATTAGCCGGGATGGTGG

R271 CTTCTTTACTGAGTCTTCTAAAGC

R272 TGTCCCTTGAATGTAGGTATGTGG

R273 GGATCTGCAATACTGACATCTCC

R274 ATTGAAAAGAACTGAAGGATCTACC

R275 GTGAGCTGAGATCTCGTCTGC

R276 TTTGTCTGAAACAGATTCTAAAAGTGG

R277 GCAGGTCCTGTAGTCCCAGC

R278 GTTTGAGCTTCTAAAATTGATGGATT

R279 GTGGTAGGTCAAACCGCAATCC

R280 ACCAAATCAGACATATCAGCTTGG

R281 CACAGAACGGATCCTCAATAAAGG

R282 GTTAACTCTCCCTCTCTTTATGG

US 9,145,587 B2

**35**

282 Reverse ABL Primers Used for the Second PCR Round and the Tag Sequence which was on the 5' End of Each Primer

2nd Round  
Tag D gtgttcagagagttgatttccagg

RN1 cccacttgatTTTcccacatgg

RN2 atttatttagatgaagtgaatatttcc

RN3 atttagttgttaactgtgagtgc

RN4 gtacagaagtgttgcatacc

RN5 aggcaaaaaatttccatttagc

RN6 acaagcacgagccacagcacc

RN7 cgctttgttgcaggctgg

RN8 cccaaaacagacttttagataacc

RN9 ttcaaattgttttttactcacc

RN10 gatctaaaaaaagtgcacagggttgg

RN11 cactaaaatttgaaggAACatgtgg

RN12 tctggcagttggctctagg

RN13 accataagtggtttacctgtgg

RN14 cccaggcgcagggtattctcc

RN15 ggtggctcacgcctgaaatcc

RN16 cacagtccacgtgccacaatcc

RN17 aatcatgttaacacatccctctcc

RN18 gaagagagtgttgcAAAGGTTAAGC

RN19 cgagaccataactggcttaagatgg

RN20 attagccacacaataatgttctgg

RN21 tttaaaaAGCGTTGCAATATGATGC

RN22 ggTTGCAgTgAgCCGAGATCG

RN23 ggtggggaggactgcctgagc

RN24 aacagagagaaaaacacaaattacc

RN25 gatATCTGAATTCCAAATACTTGG

RN26 gtgatAGAATTAAAGGAAAAATAACG

RN27 attgttccTTTCTAAATATTCTACC

RN28 cagcaCTTGGGAGGCTGAGG

RN29 cacagAGGTTCACAGTGTGG

RN30 aacttCTGTTGTCCATAATGC

RN31 gcCTGTAATCCAGCACTTGG

RN32 gccAGTAACATGAAAAGGTGC

RN33 aattatgtAAATAAGAGTGAAGG

RN34 cccCTACACAGAAAAACAATTCC

RN35 tgagtgtCAAAGAAAAATACTTGG

RN36 atacacAGAGAAAATGAGTCCACC

RN37 aacACTCCCCTCTGTGG

**36**

-continued  
gatattcttgcAACCTAGGATGC

RN39 ctctaaaactaatcAGCAATGTAACC

RN40 cacCTGTAATCCCAGCACTTGG

RN41 cgtaaaACTGCCACAAAGCTGTAGG

RN42 gtggcAGAGGTGCAAGCAAGC

RN43 acagAAATGACAAACGCATGTACC

RN44 acactCTCTTAGCTAGGCTTGG

RN45 gagCTTGGAAATAGGGCAGTTC

RN46 ctgggttcttAAACATGTCCAGG

RN47 tcaagAAAGGACACTGCAGTGGC

RN48 catgcACACAAACTATCTCATTC

RN49 tagCCGGGcatGGTGGCACG

RN50 atcatGCTATTGAAATTCAAATAGC

RN51 ttggcatgcAGGGCAGTGCACC

RN52 ggtggTgAGATAAAACACCTGC

RN53 ttgttatataataatcatttGATCC

RN54 cggtaACTGTTACTCTGGGATGG

RN55 aggctAGGTTCCCTCTTCC

RN56 gtagtgcCTAGCAGAGAAAGC

RN57 ctAGCCTGGCAACAAGAGCG

RN58 tctctCTCTCTGGGATCAG

RN59 gtttGAATATTGATGCAAGCAAGC

RN60 tagAACAAATTCTGGCTTATAAAAGC

RN61 ccactCTACCTTATTCTTGCC

RN62 agaccAGAAATGCAAGCAGAGG

RN63 ggacgtttGCTGGTGTCTGCG

RN64 aAGGAACAAACTGTTGTCACATGC

RN65 atgtAGCTGGGACTACAGGTGC

RN66 ggCTCATGCCTGTAATCCCAGC

RN67 atgaggTTTCAACACAAAAGATGC

RN68 tgggcGACAGAGCAAGACTCC

RN69 aaATGTCCCTAAAGTGAATCAACAGC

RN70 cAGACTCAGTTTACCTCATCAGC

RN71 agtGATCTTCTCTTTAACCTCC

RN72 ccAGCTATTCAAGGAGGCCAAGG

RN73 cttaAACATTATGACACTGTCTTG

RN74 ccAGGTCTATGAGGCCGTCC

RN75 tccAAAGCATCCCTACATTATCC

RN76 acatacatacATGCAGTGACTAGC

RN77 tacAGGTGCCAGCCACCATGC

RN78 gcctGTAATCCCAGCACTCTGG

## US 9,145,587 B2

**37**

	-continued	
RN79	gacagagtcccactttgtgc	RN119
RN80	gtgccttccaaaggcagtgttagg	RN120
RN81	tatcttactgggtatgtataatgcc	5 RN121
RN82	caaaggaaatacgtcctaccagg	RN122
RN83	ccttttctcacagacatgttcc	10 RN123
RN84	taaacacagtgcgcagaatccc	RN124
RN85	ataaagcaaaactctaaaagggtcc	RN125
RN86	accactacactccagcctggg	RN126
RN87	gataacctgggtcagagtaagtgc	15 RN127
RN88	tgtatatctcagtcacttgggagg	RN128
RN89	gtgtcgcttctttctctacg	RN129
RN90	ctggcttagtatgagggtggtgc	20 RN130
RN91	ggacttagccacatttcaaccagg	RN131
RN92	gcagttatactgagaatttagttcc	RN132
RN93	gaggctgaggcaggagaatgg	25 RN133
RN94	cattgttgatgaaggtaacacgc	RN134
RN95	cagacaagagtggctacggcag	RN135
RN96	acgcccagccagattattcagg	30 RN136
RN97	ggaaccagaaagaagtgc当地	RN137
RN98	ttagccatcttggaggcaggc	RN138
RN99	caggaccttcatacaaaccctcc	35 RN139
RN100	aacacaacatctgaccttaacgc	RN140
RN101	gccttagaagtccagaggaaagc	RN141
RN102	tgacgtacccagtagacatttcc	40 RN142
RN103	ctctgcaaggcctggaaacagg	RN143
RN104	gccttgtccccaaagtcttaagg	RN144
RN105	gcaaaggactctgaaattcc	45 RN145
RN106	gctcctgcctgtaatcccagc	RN146
RN107	gaaggaaaacagaaaaaagcagaggc	RN147
RN108	cttactaccgtttttcttcactgg	50 RN148
RN109	actattctgttttttagtttactgc	RN149
RN110	cggtgctcacacctgtaatcc	RN150
RN111	agccagagttctgtgtctagg	RN151
RN112	taatttgcatttcgtgcgcgtcc	55 RN152
RN113	cacttttaatacagatcccaatagg	RN153
RN114	atgtatttttttttctgtcaagc	RN154
RN115	aaatgttaacattatttccctaagg	60 RN155
RN116	catatgcccagatccgtctcc	RN156
RN117	acaggtgtgagccgctgcacc	RN157
RN118	gccaagacgtttacagtttggc	65 RN158

**38**

	-continued	
	aggaaacttctgaggatgtggg	
	gctttatagggcagtctgaattcc	
	ttagaataaaagtatctcgggagg	
	taatttctcagctttatccctcag	
	cacatgactaattcttattcattcc	
	aaagacctcaagaaaagagtcccc	
	gaccataaagattatatgcccag	
	aaagtactaatgcagtgtgtcagc	
	gaggttcctcgattccctgc	
	ggagagcagaggaattcacagg	
	agtaatttagaaactgattctaagacg	
	cataccattgccaatccagttcc	
	attacgggtgcctgccactgc	
	cagccaggcagaggagagagg	
	ttttcattccaagttctgtttggg	
	tttcaataggaatttggataatccc	
	taagccgagatcacaccactgc	
	ccttcagcgcattatacttggc	
	ccatctaattccatcttaatttcc	
	gagtgagactgcgcactgc	
	aatcatgtgc当地attaaaccatggc	
	cccagggaccagaccagacc	
	ctcaactcaccagtgaaaatcagc	
	ggttgctctcgactcctgacc	
	gttccccagctccttctgc	
	agaaaagatgtagaagggtccagc	
	ggggaaaagggttattatgc当地	
	ctctctcagacctaattgc当地	
	aactatacatacagtatttgattagc	
	aaattaatgc当地attccatgtccagg	
	cttttccactctaagagaaccc	
	ttttggtggttcatattggctgc	
	gcttccacaaaatgc当地acaaaagg	
	ggctcatgtttgtatccaggc	
	catatgaaattttgttccctttagg	
	cactggtacaagtccaaagatcc	
	gaccctgtgtacttccctggg	
	tatttgaactatcttgc当地atgtcc	
	ctgattaaaaagtattacccttggc	
	tttggaaactgc当地actcaataacttgg	
	agtaatgtgtcatgtccaaatggc	

## US 9,145,587 B2

**39**

-continued

RN169	gaaagcattcccaatgtctcacc	RN200	tcccagggtcaagccattctcc	
RN161	caatggacaaaaggcccaactgc	RN201	tatTTTgagagtctcactctgtcg	
RN162	tccagctctggcttttggtaag	5	RN202	gtctcgaactcctgacctcagg
RN163	acggaggtctcaactccgtgacc	RN203	aaggaggtgaagagtgaactacg	
RN164	ctatgtcatagtcagaagagactttgc	10	RN204	gtctcaggTTTggacttacttgg
RN165	gttcaagcgatttcctgtctcg	RN205	tttacagatcttaaatgcattaggac	
RN166	ccacctaataacttaaatacggaagc	RN206	gtacactgaacaaaaggagacagg	
RN167	atattcaacaaaacttaatagtgaagt	RN207	ctggtagtaatgcaaaatagcacc	
RN168	ttacaggcgtagtccccatgc	15	RN208	catttaatgtgaaatgaattataagcc
RN169	aacacctccaagggccaaacg	RN209	gagacagggtttcactatgttgg	
RN170	tactattggcaaattcaatttatatgg	RN210	ccagcacTTTggaaaggctgagg	
RN171	agccccacatcctaaaattcaataag	20	RN211	gaaaccaagtatcatggtaaattgc
RN172	gaaagtggataagtgtttgtctgg	RN212	cagtgagggtctgctcagttcc	
RN173	ggccaggcattcaagaccagc	RN213	gccaggtgcggTggctcacf	
RN174	agccaacaacaaaaagacacaacc	25	RN214	catgcctgtatcccagctacc
RN175	ttgagcccaggaggatccaagacc	RN215	atgtaaatggtagactcactttagg	
RN176	cagactaaagatctcagagagaaac	RN216	cccacaatacagagaactcttacc	
RN177	cgcttgtaatcccaggacttgg	30	RN217	tgaaacatgcagcccagtgtcc
RN178	aaaagtgaaatcagaatttgg	RN218	tgtttttctccctgccttcaatcc	
RN179	caggcgtgagcaactgtgtcc	RN219	gctttcctgggtctccatctgg	
RN180	ggccaggtaggtctcggttgc	35	RN220	gcagccgcttgaaaacaaaacagc
RN181	actttgaaatgtgttatagtgg	RN221	gatcacgttacatttgggggtgg	
RN182	ttccctgtcatctaagtcttctcc	RN222	taggtgaaaaactaaaatttgg	
RN183	agatatctaccattgaagagttgc	40	RN223	ctcccttggctcttttagtcc
RN184	agtcttcacttcacttgg	RN224	gcctccggctccaaagtgc	
RN185	ccatgcaggatgaaataaaaaagc	RN225	aatgcctagagagatTTggcagg	
RN186	tgggtgacagagtggactcc	45	RN226	gagatggggTTTcactatgttgg
RN187	acagcaataccgggttaacatgc	RN227	tgtgatcttgcactgcactcc	
RN188	tttatgtaaaagatgaatgcgg	RN228	acttctccatTTgttttcc	
RN189	ctactctgtactggaaacagg	RN229	cgtccccggctcagttctac	
RN190	caaacgttagtctggaaatgcg	50	RN230	ccaaaacaataaaaatcacaatttgg
RN191	tgcacgctaccacacccagc	RN231	ctgaactgccttagatgaaatccg	
RN192	aattcttggatctgtgtttactgc	RN232	atTTCTGTATCAGGTCTGTGTTCC	
RN193	taccagttatcattctttctgc	55	RN233	ggctgacccttcaactgttcc
RN194	atccacccacccggctcc	RN234	aaaaattagccaggcatggtgg	
RN195	cactctgcctggcccttaatgg	RN235	gcagtgagcagtgtcgcacc	
RN196	atagttgttaatatgcactaagg	60	RN236	aaagactgtgaactaactgttgc
RN197	gcgtgagccacccgacctgg	RN237'1	tgccaagaattacacattattagc	
RN198	ctccatcacacaaaattttatgtggc	RN238	ggccaggatgtcattaacttcc	
RN199	agacggagttctcggttgc	65	RN239	gtaagagctgacgtgtattgtgc

**40**

-continued

RN200	tcccagggtcaagccattctcc		
RN201	tatTTTgagagtctcactctgtcg		
RN202	gtctcgaactcctgacctcagg		
RN203	aaggaggtgaagagtgaactacg		
RN204	gtctcaggTTTggacttacttgg		
RN205	tttacagatcttaaatgcattaggac		
RN206	gtacactgaacaaaaggagacagg		
RN207	ctggtagtaatgcaaaatagcacc		
RN208	catttaatgtgaaatgaattataagcc		
RN209	gagacagggtttcactatgttgg		
RN210	ccagcacTTTggaaaggctgagg		
RN211	gaaaccaagtatcatggtaaattgc		
RN212	cagtgagggtctgctcagttcc		
RN213	gccaggtgcggTggctcacf		
RN214	catgcctgtatcccagctacc		
RN215	atgtaaatggtagactcactttagg		
RN216	cccacaatacagagaactcttacc		
RN217	tgaaacatgcagcccagtgtcc		
RN218	tgtttttctccctgccttcaatcc		
RN219	gctttcctgggtctccatctgg		
RN220	gcagccgcttgaaaacaaaacagc		
RN221	gatcacgttacatttgggggtgg		
RN222	taggtgaaaaactaaaatttgg		
RN223	ctcccttggctcttttagtcc		
RN224	gcctccggctccaaagtgc		
RN225	aatgcctagagagatTTggcagg		
RN226	gagatggggTTTcactatgttgg		
RN227	tgtgatcttgcactgcactcc		
RN228	acttctccatTTgttttcc		
RN229	cgtccccggctcagttctac		
RN230	ccaaaacaataaaaatcacaatttgg		
RN231	ctgaactgccttagatgaaatccg		
RN232	atTTCTGTATCAGGTCTGTGTTCC		
RN233	ggctgacccttcaactgttcc		
RN234	aaaaattagccaggcatggtgg		
RN235	gcagtgagcagtgtcgcacc		
RN236	aaagactgtgaactaactgttgc		
RN237'1	tgccaagaattacacattattagc		
RN238	ggccaggatgtcattaacttcc		
RN239	gtaagagctgacgtgtattgtgc		
RN240	cccggtgaggccgcacatcc		

US 9,145,587 B2

**41**

	-continued
RN241	cctgcgcctaaccctcc
RN242	cggcgcttagggccatcg
RN243	acttaaggaaacgaacatgacacc
RN244	gagaccgagtcttgctgtcg
RN245	gtattaattgaagatgatttggatge
RN246	tctttaaaagactatcgctggac
RN247	aaaagagacatcagtagagcatcc
RN248	gttcatgtttcttgcgtctcc
RN249	tttcgaaagttcaggctgagtgc
RN250	gaccctcaaaacaatccctcaagg
RN251	caaaacacacttagaaacaaactgc
RN252	gcctgggcacatagtggac
RN253	ggcaggagaatggcgtgaacc
RN254	tttgctcggtgccaggctgg
RN255	gcaacttaatgtgatagaataatgc
RN256	cctcccccctctgtgcgc
RN257	ccacaacaatgtaaactctctgg
RN258	tactcccttagatgttgtccc
RN259	gggtcccccttggccattcc
RN260	gatctggctacttcaacctcc
RN261	aggggaaatatttaaaccttgg
RN262	aatgcaatggtgcatatcacagg
RN263	tcatttatctatttctacatggtcc
RN264	ggaaggaaatggccatgaaacc
RN265	agtgaacatttctgcagccctcc
RN266	caacaggacgtcaggcgatcc
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RN270	gcatgcctgtaatccaaagctgc
RN271	gaaacaattcttttccacacttgc
RN272	ggctcatgcctgttatcccagc
RN273	agaagaagcttagtcatatgtttgg
RN274	cagatgcttgagccaaacaaatgg
RN275	ctggcagacagactgagactcc
RN276	aatgtgtgaatatttattacagg
RN277	gcaggagaattgttgaaacctgg
RN278	ctttagtcaaattaaaacagtctatcc
RN279	gatttctatctctgcacaccacc
RN280	ttcttgcgttaactactaaaaatctcc

**42**

	-continued
RN281	aaagggtcttcataaggctaattgg
RN282	ctcttaaggatttttatatgaagacc

5

Example 3

Identification of the PML-RARalpha Breakpoint

- 10 Amplified patient DNA was electrophoresed on a 2% agarose gel. P is patient DNA, N is the normal DNA and W is the water control. The patient DNA was amplified using multiple RAR $\alpha$  primers and a single PML primer
- 15 a) Amplified patient DNA electrophoresed on a 2% agarose gel, P is patient DNA, N is the normal DNA and W is the water control. The patient DNA was amplified for one round using an RAR $\alpha$  primer and a PML primer designed using the breakpoint sequence.
- 20 b) The sequence chromatogram obtained from the patient DNA. The breakpoint between PML and RAR $\alpha$  is shown.
- Isolation of the PML-RARalpha Breakpoint in Acute Promyelocytic Leukemia
- 25 Two patients have been studied and the breakpoint has been isolated and sequenced in both. The primers used are shown in Example 4.

Example 4

30 Primers Used for Isolation of PML-RARalpha Translocation Breakpoint in Acute Promyelocytic Leukemia

35 PML Forward Primers

	1st Rd	
RN263	PML F1-FT1	caggaggagccccagagc
RN264	PML F2-FT1	tcctggggatgggtggatgc
RN265	PML F3-FT1	tgaccccacagatgttacacago
RN266	PML F4-FT1	agtcaaggcaggctctgcc
RN267	PML F5-FT1	tatttggccccatccagaaagc
RN268	PML F6-FT1	cacccagagtagacgttggatcc
RN269	2nd Rd	
RN270	PML F1-FT2	gaggagccccagagcctgc
RN271	PML F2-FT2	tggggatgggtggatgttacc
RN272	PML F3-FT2	cccacagatgttacacagctgc
RN273	PML F4-FT2	caggctctgcccactcacc
RN274	PML F5-FT2	ccatccagaaaagccccaaagcc
RN275	PML F6-FT2	ccagagtagacgttggatcttcc

60 The second round primers were internal to the first round primers and were used for performing Bottleneck PCR in order to eliminate non-specific amplified material and facilitate isolation of the translocation breakpoint.

Various combinations of the forward and reverse primers can be used. 2 exemplary protocols were either to set up 6 PCRs, each containing a different PML primer and all 34 RARalpha primers, or to set up 1 PCR which contained all 6 forward and all 34 reverse primers.

34 Reverse RARalpha Reverse Primers Used for the First PCR Round and the Tag Sequence which was on the 5' End of Each Primer

Tag R1	gcagtacaaacaacgcacagcg
RAR1	ctgccaccctccacagtc
RAR2	gccaagaccatgcatgeg
RAR3	cccaggacaaagagactccc
RAR4	caggaagcagacagtcttctagtcc
RAR5	tgcctgtaatcccaacactttgg
RAR6	tccctctggccaggatggg
RAR7	atggggaatggggatggaa
RAR8	cagatcgttctccctccacgc
RAR9	acaaaaaaaacatgtcagagagg
RAR10	tggtgcatgcatctgttagtcc
RAR11	aggtgtctatacatgttagatccc
RAR12	ccaggacaggatggagatctgg
RAR13	agggaacctgtgcattatccttc
RAR14	cagaagtcttgcattttagggagg
RAR15	gggtacgtgaaactccacaaagg
RAR16	cagagtgtggcaagcaagg
RAR17	aacatttaaaggtaaaataacgtggg
RAR18	tagggagcaacagccattaagc
RAR19	ggtgcaactgtccagctctgg
RAR20	actctcgctgaactcgcctgg
RAR21	ctcggtctctgggtacgc
RAR22	gcaaggaggctcgagctggg
RAR23	ggaagaagtgaaacaagagatgaa
RAR24	cccagagaacaaaccggattagg
RAR25	cccttcaaccttctccaaatctgc
RAR26	cccatgtccagtggttaggg
RAR27	gagattgggtggagacagatgg
RAR28	cttctcagctcaaaggcttcagcg
RAR29	gaatgggagagatgaccagagg
RAR30	aaggcaagggggtatgtgg
RAR31	ggaaggaaaggcatggaaacacc
RAR32	ccatcaatgctctgtctgtctgg
RAR33	gtgcgtgactgtgttgg
RAR34	acatccccattgacccatcaagc

Nearly all translocations involve a 3 kb region of the BCR gene and 140 kb region of the ABL gene. Six forward primers used to cover the region of the BCR gene and 282 primers used to cover the region of the ABL gene. Six PCRs are set up, each containing one of the BCR primers, all of the ABL primers, and the common tag primer.

If necessary, a second round of PCR is performed with a nested internal BCR primer and 282 nested internal ABL primers Alternatively, 1-3 rounds of Bottleneck PCR are performed in order to remove non-specific amplified products and reveal the amplified translocation sequence.

The ABL gene is very rich in Alu sequences, and the BCR gene also contains one such sequence. The ABL primers have therefore undergone a selection procedure which sequentially involves, for each ABL primer:

design using standard criteria  
pairing with each BCR primer and testing by electronic PCR for amplification off the BCR template. Primers that fail this criterion are discarded.

incorporation in a pool of 12 or 24 ABL primers, pairing the pool with each BCR primer, and testing by experimental PCR using a BCR template which has been previously produced by PCR amplification. Any pool that produces amplification and thus fails this test is further analysed by testing each of the individual ABL primers to determine which is responsible for amplification. When identified, this primer is discarded.

25 The BCR and ABL primers used in Example 1 are shown in Example 2.

Those skilled in the art will appreciate that the invention described herein is susceptible to variations and modifications other than those specifically described. It is to be understood that the invention includes all such variations and modifications. The invention also includes all of the steps, features, compositions and compounds referred to or indicated in this specification, individually or collectively, and any and all combinations of any two or more of said steps or features.

TABLE 1

Sequence Identifier Sequence		
	SEQ ID NO:001	gtggggccccccgtttccgtgtacaggcac ctgcaggaggggcaggcagctagccgtaaagg ctgatcccccccttctgttagacttttgat gggactatgtggactttgggttcagaaggaa gctatgtgttagggcccttgcctcc caggatggacaagggtgggttaggacagg tctccctgatggctgc
40	SEQ ID NO:002	caccacgtctggctaattttgtatTTT tagatgtgggttcaacatgtttagccagg tggatcgactctgtacccgttgc ccccctggccctccaaatgtgtgggat caggcaggagccactgtgcggccgtgac catatttgaataccgagttttatgttgc gacgtcaggatggatggaaaggaaacac ttgatttccatcgacgcacaggccgc tctgaatggatgtgcacgtgtgc gcacactacacacacgtacacacacatca caaataactgtgcggccgtgacccatatt tgaataccgagttttatgttgc cagg
45	SEQ ID NO:003	tttggggaggctgaggcagggtggatcgcttga gtcaggatgtggagaccaggcgtgaccaaca tggtaaacccctgtgtactaaaaatacaa agattagccggctaggcagtgccggcactgt aatcacaactgtggggatgtggggatggaa gaatcgcttgcacccaggaggccggagg atgtggcccgatgttgc cctggcgcacagag
50		
55		
60		

45

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:004	ggcttcactctgttgaactcctggcctca aagggatcccttacactcggtcacaaagt atggaaattacagggtgagtcaactgcagct ggccttcaacttatcaactgtgaggagtaaca gctgcatgggtggcttaatgecatctaacad gagtactccatgtcagacagtaggtatcac aatgattattata>tagaataggccac agttacatagactaaggagccatcccgtc t
SEQ ID NO:005	cctccagctaccctgcacgggcac tcaagtggtttgcattcaacttgtgcacata tgctcagtcacacacacagcatacgtatgc acatgtgtccacacacacccccacatcc cacatccccggacccccctgtgccttg gaaccttattacatttcgactgtgttgc cctgtattgtgaaaccaggctggatcc
SEQ ID NO:006	ttatttataacaacatttcagcgtggcaac tgcagtttcaagaatggtaataccatgt cagagagatgcaatgataaaaataggaa agaaagcagggtgtctggccagaggaccaga ttaaagaacccatgagactacaatgtt atgtaaaatgggtcttcgtcaaaatcatgt ctacagaagctgtt
SEQ ID NO:007	tgcacccatataacataatcttcgtgg ccctgtctgtgcctcataaaacgtgg tggccctctgtggcctccgtcatccctg catctctccgggtctgtctgtgacat acacgcgtacacccatgcgtccccgtgg ccgggttgccttcgtccctgttac ctttttctatcttcgttgc
SEQ ID NO:008	gtgagctccgcctctgtcagatcagtgg gattagtttctcataggagcatgaatcta ttgtgaacagtcatgcgtggatcagg gctgtccatgtgagaatcta gtctctcattgtcttactccatgt aggactgtctatgtcaggaaaaacaatgtca gggtcccaactgttacattacagtgg tgtataattatataattacaatgtataaa taa
SEQ ID NO:009	ggagtctgaggaggggaaaggaggcaagg gctcgatcccgccagtaagtcgggtgt g
SEQ ID NO:010	cttctccctgacatccgtgg
SEQ ID NO:011	acacagcatacgtatgcacatgt
SEQ ID NO:012	gaggtttgcagatgaccacgg
SEQ ID NO:013	cagctactggaggtgtcagaacac
SEQ ID NO:014	tgggcctccctgcattcc
SEQ ID NO:015	tccccctgcacccacag
SEQ ID NO:016	tgacatccgtggagctgcagatgc
SEQ ID NO:017	acatgtgtccacacacacccacc
SEQ ID NO:018	accacgggacaccccttgcacccgttgg
SEQ ID NO:019	ctggagctgtcagaacagtgaaagg
SEQ ID NO:020	tccctgcattccatctccatcc
SEQ ID NO:021	cccacgacttcccgactgagc
SEQ ID NO:022	gcaacactgtgacgtactggagg
SEQ ID NO:023	gtctatctaaaattcacaaggatgc
SEQ ID NO:024	aggcaaagtaaaatccaaggaccc

46

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:025	cactcctgcactccagcctgg
SEQ ID NO:026	caaccaccaaaagtgccttcctgg
SEQ ID NO:027	atatggcatctgtaaatattaccacc
SEQ ID NO:028	tgcctcgccctccaaagtgc
SEQ ID NO:029	agccaccacacccagccagg
SEQ ID NO:030	aataactgttttcccccacaaac
SEQ ID NO:031	tgttttacaaaaatggggccataacc
SEQ ID NO:032	acttaagcaaaattcttcataaaaagg
SEQ ID NO:033	cttcaattgttgcacactctcc
SEQ ID NO:034	acccctgcacatctctcccttgc
SEQ ID NO:035	aaataaaagtggatcataactgg
SEQ ID NO:036	caccatcacagtcactgcagc
SEQ ID NO:037	aacctcttgcataatcgatagcc
SEQ ID NO:038	aaataaaagtacatacccaatttgc
SEQ ID NO:039	gacacattccatgggttattcc
SEQ ID NO:040	tgtaaaatatggttcagaaggagg
SEQ ID NO:041	gcagggtgataacgaggcagg
SEQ ID NO:042	ccagccaagaattcaaagattgc
SEQ ID NO:043	gaaggaggatgacaaaggaaacg
SEQ ID NO:044	gcagaagaactgttgcacactgg
SEQ ID NO:045	gtggcccgactactcgagagg
SEQ ID NO:046	ccctcagaaaaactaactgaaaagg
SEQ ID NO:047	tagaaaccaagatatctagaattccc
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SEQ ID NO:059	aggcatccatcaggattatggctcc
SEQ ID NO:060	cctgagtaacactgagaccctgc
SEQ ID NO:061	aacactcaagctgtcaagagacac
SEQ ID NO:062	attcaggccaggcgcagtg
SEQ ID NO:063	taaatcgtaaaaactgcacaaaagc

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:064	cagaggaggtaggagaaggaaaagg
SEQ ID NO:065	ggtagctatctaccaagttagaatcc
SEQ ID NO:066	atccatggaaaaagtcaccaaagc
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SEQ ID NO:071	ctggccaacatagtgaaaccacg
SEQ ID NO:072	atttgaataggggttaaagtatcattg
SEQ ID NO:073	cacttcagtggaaagtggcatgc
SEQ ID N 0:074	gtttttcttgcagaatgtataaacatcg
SEQ ID NO:075	gctccttagtctatgtacctgtgg
SEQ ID NO:076	tactctggcatggtaactgtgtgc
SEQ ID NO:077	acaaaggacttaggtctgtggagc
SEQ ID NO:078	ccaagtttaccaaattaccaaagttacc
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SEQ ID NO:098	catgttggccatgttctgtgagg
SEQ ID NO:09	9 ctcagcctcccgagtagctgg
SEQ ID NO:100	aaagacatttaaagaggagatgggc
SEQ ID NO:101	tgctgggattacaggcgtgagc
SEQ ID NO:102	tgtgacttccatccgcagctcc

TABLE 1-continued

Sequence Identifier	Sequence
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SEQ ID NO:106	tggcaaaatgtatcgagctgcc
SEQ ID NO:107	tatgaacacagccggccatcagg
SEQ ID NO:108	gaggttgcagttagtgcgatcg
SEQ ID NO:109	gtcaagcacccagtcggatacc
SEQ ID NO:110	atctggcttggcggcggcggc
SEQ ID NO:111	gttaagcgggtccccatcaggc
SEQ ID NO:112	cagccagtttcagtagaaagatgc
SEQ ID NO:113	gacccaagcataagggactagc
SEQ ID NO:114	cccaaaaagttacaagagaaaatttc
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SEQ ID NO:131	agttattgtatctaactataacaacgc
SEQ ID NO:132	aaagactaggggccggggacgc
SEQ ID NO:133	ctggtagaaataaagacacaacaaagcc
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SEQ ID NO:137	ggcaggaaatactgtgttcaag
SEQ ID NO:138	gtggtaatccacccactcagttacc
SEQ ID NO:139	tcccaaagtgcggattacagg
SEQ ID NO:140	aaaattgcacaaatgcggcaagacgc
SEQ ID NO:141	taagtattggaccgggaaggagg

49

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:142	ctatcatttgtctcaaagtgttagcc
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SEQ ID NO:146	acttcacaccaggcgttgcacc
SEQ ID NO:147	taactcatatcctcagagagacc
SEQ ID NO:148	agagggttcctcgattccctgc
SEQ ID NO:149	gtgtcagcgtccaaacacaaaagc
SEQ ID NO:150	gaaagtggatgggcaagcattgc
SEQ ID NO:151	gtgatcacctcagactgcagg
SEQ ID NO:152	gtttgttagtcaaggcattcacc
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SEQ ID NO:156	agctggcaaacttggtaataaaaag
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SEQ ID NO:158	gcaggcatgtaagacccatc
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SEQ ID NO:162	ccaaccacacttcaggggatacc
SEQ ID NO:163	cacgccatgcaactgataactc
SEQ ID NO:164	gggtttcacatgtggccagg
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SEQ ID NO:171	gaaacggcttggatcaatgtatcc
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SEQ ID NO:173	ggcctccgtttaactgttgtgc
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SEQ ID NO:176	gcaaaagccaaagagccccctgg
SEQ ID NO:177	ttctccaaaatgagcccaagg
SEQ ID NO:178	gtggtgacgtaaacaaaaggatcc
SEQ ID NO:179	gcaaattccatgtgaatcttattggc
SEQ ID NO:180	cctgatctatggaaacagtggtgg

50

TABLE 1-continued

Sequence Identifier	Sequence
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SEQ ID NO:182	gaaccccgtaacagtgtatcacc
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SEQ ID NO:184	catacctaaaatagaaatgttatccc
SEQ ID NO:185	gagttgcataatgttttataatccc
SEQ ID NO:186	tgagcccacatccataaagtttagc
SEQ ID NO:187	accgcaacctttgcgcctgg
SEQ ID NO:188	taaatatttgtatggagtaccacc
SEQ ID NO:189	aaagccaggagaaaaagttatgagg
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SEQ ID NO:194	acaaaactacagacacagaaaatgg
SEQ ID NO:195	tttgggaggctgaggttagtgg
SEQ ID NO:196	aaagacagtgaaacatctataaggg
SEQ ID NO:197	cattttggagaccaggcagg
SEQ ID NO:198	gcatggacagacacaaagcago
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SEQ ID NO:203	gaaggtttattcatataaaatgtgcc
SEQ ID NO:204	ctggcttctgtggtttagttgg
SEQ ID NO:205	acagacatccatcttaaggatgg
SEQ ID NO:206	gctagctttgtgttaagaatggg
SEQ ID NO:207	ggcctactcacacaatagaatacc
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SEQ ID NO:215	cctgggtggctccagtttctacc
SEQ ID NO:216	aactcctgacactcatgtatccacc
SEQ ID NO:217	gctgggattacaggcatgagcc
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SEQ ID NO:219	tcccaaagtgtggattacagg

51

TABLE 1-continued

Sequence Identifier	Sequence
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SEQ ID NO:224	ttcaccatgttggccaggctgg
SEQ ID NO:225	catcaactgaagatgacaactgagc
SEQ ID NO:226	gtccagcctggcgatagagc
SEQ ID NO:227	gaggaaagtctttgaagaggaacc
SEQ ID NO:228	ggtacactcaccagcagtttgc
SEQ ID NO:229	gagcaactggtgtgaatacatatgg
SEQ ID NO:230	caataacctggcaccacatacacc
SEQ ID NO:231	gggactacaggcatgtgccacc
SEQ ID NO:232	cggtggtcacgcgttaatcc
SEQ ID NO:233	caactgttaaatctctatggaaacc
SEQ ID NO:234	gacaaaggattagaaaatgcaccc
SEQ ID NO:235	ggaaatgttctaaaactggattgtgg
SEQ ID NO:236	aataataatagccagggtgttagc
SEQ ID NO:237	ctggaacactcacacattgtgg
SEQ ID NO:238	ctgggtgacagagcgagactcc
SEQ ID NO:239	cccaaatcatccccgtgaaacatgc
SEQ ID NO:240	gaccctgcaatccaaacactgg
SEQ ID NO:241	ctctcaggccttcaaactacacc
SEQ ID NO:242	caggaaaggcgtcgctcagtgg
SEQ ID NO:243	atctgaaaagcagcagcagg
SEQ ID NO:244	gtaccatgacagacaagtttagg
SEQ ID NO:245	cttatcccctactgtctcccttgg
SEQ ID NO:246	ggatggtctcgatctccctgacc
SEQ ID NO:247	aggttagagaccccttcataatgc
SEQ ID NO:248	agctgggattacagggtgcctgc
SEQ ID NO:249	gctgaggcagggtgggctgc
SEQ ID NO:250	acatttaacgtctcctaacttctcc
SEQ ID NO:251	gtgctgcatgattacagggtgtgagc
SEQ ID NO:252	tatgacagcagttataactatcacc
SEQ ID NO:253	ctggggaccaaatctgaactgcc
SEQ ID NO:254	gtagctattgttattccaaaagagg
SEQ ID NO:255	gcttgggacccaggacaagg
SEQ ID NO:256	cctggccaacatgggaaatcc
SEQ ID NO:257	aattgcttgaacactggagggtgg
SEQ ID NO:258	gcctaagacccaaaagctttagc

52

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:259	catattaaaggccatattcaaattgg
SEQ ID NO:260	ggatgttaaccagggttatcacagg
SEQ ID NO:261	ggaagtttagtccacatcttctagc
SEQ ID NO:262	geacccacaggacaaccacacg
SEQ ID NO:263	gggacgcgcctgttaacaagg
SEQ ID NO:264	gggctggggccacgctcc
SEQ ID NO:265	cgoaaaagtgaagccctctgg
SEQ ID NO:266	gaaatcctacttgcataaagtgcgc
SEQ ID NO:267	ttttagacaacttggaaaaataagcg
SEQ ID NO:268	ttcccaaaagacaaatagcacttcc
SEQ ID NO:269	ccattttggaaaatcacagtgtattcc
SEQ ID NO:270	gaaaagaaaaccctgaattcaaaagg
SEQ ID NO:271	tgctaaaaagaagcattaaaagtgg
SEQ ID NO:272	ctcttaccagttcagagcttcc
SEQ ID NO:273	ttttcagccaaaaatcaaggacagg
SEQ ID NO:274	ctttagcccaggagtttagacc
SEQ ID NO:275	cgcctgttagtaccctctactagg
SEQ ID NO:276	ggtaaaagaagaaggattgaaaacc
SEQ ID NO:277	taagagtaatgaggtaaagtttatgc
SEQ ID NO:278	catttttattgtcacaggccatttgc
SEQ ID NO:279	gecacgcctcttcttgcacc
SEQ ID NO:280	tgcctctctgactgcactgtg
SEQ ID NO:281	ccatgcttaccacgccttgg
SEQ ID NO:282	cattcaggctggagtgcgggtgg
SEQ ID NO:283	ctaaaaattgtctggtaagacattg
SEQ ID NO:284	ttgctttgttgcgggttgg
SEQ ID NO:285	gagcttagaggaaaagtattatttcc
SEQ ID NO:286	ttggtgctgtgccagacgttgg
SEQ ID NO:287	cagatctttggctattgtcttgg
SEQ ID NO:288	gaaggaaaggcctccactgc
SEQ ID NO:289	cataaaaaagcatgtgggagg
SEQ ID NO:290	caaacataaaaaagctttaatagaagacc
SEQ ID NO:291	tcccaactatgaaaaatagaagacg
SEQ ID NO:292	cacaaattagccgggcatggtgg
SEQ ID NO:293	cttcctttactgagtcttctaaagc
SEQ ID NO:294	tgtccttggaaatgttaggtatgtgg
SEQ ID NO:295	ggatcttgcataactgacatctcc
SEQ ID NO:296	atttggaaaagaactgaaaggatctacc
SEQ ID NO:297	gtgagctgagatctcgctctgc

53

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:298	tttgtctgaaacagattctaaaagtgg
SEQ ID NO:299	gcagggtccgttagtcccagc
SEQ ID NO:300	gtttgagttctaaaattcatggattc
SEQ ID NO:301	gtggtaggtcaaaccgcaattcc
SEQ ID NO:302	accaaattcagacatatacggttgg
SEQ ID NO:303	cacagaacggatccataaaagg
SEQ ID NO:304	gttaactccccccttcattatgg
SEQ ID NO:305	gtgttcagagagcttgattccagg
SEQ ID NO:306	cccaacttgattttccacatgg
SEQ ID NO:307	atttatttagatgaagtgaatatttcc
SEQ ID NO:308	atttagtttgttaactgtgagtc
SEQ ID NO:309	gtacagaagtgcgttatgcatacc
SEQ ID NO:310	aggcagataaaaatttccattagc
SEQ ID NO:311	acaaggcacgagccacagcacc
SEQ ID NO:312	cgtcttgcgttgcaggctgg
SEQ ID NO:313	cccaaaacagacttctagataacc
SEQ ID NO:314	ttcaattgtttttctactcacc
SEQ ID NO:315	gatctgaaaaaagtgcagggtgg
SEQ ID NO:316	cactgaaatttgcaggaaacatatgg
SEQ ID NO:317	tctggcgcgtggcctctagg
SEQ ID NO:318	accataagtggtttacctgtatgg
SEQ ID NO:319	cccaggcgcagggtgattctcc
SEQ ID NO:320	ggtggtcacgcctgaaatcc
SEQ ID NO:321	cacagtccacgtgccacaatcc
SEQ ID NO:322	aatcatgttaacacatccctctcc
SEQ ID NO:323	gaagagagttgaaaggtaagc
SEQ ID NO:324	cgagaccatactggtaagatgg
SEQ ID NO:325	attagccacacaataatgtctgg
SEQ ID NO:326	tttggaaaaggcgttgcataatgtgc
SEQ ID NO:327	ggttgcgttgaggccgagatcg
SEQ ID NO:328	ggtggggaggactgcctgagc
SEQ ID NO:329	aacagagagaaaaacacaaattacc
SEQ ID NO:330	gatatctagaattcccaaatacttgg
SEQ ID NO:331	gtgatagaattaaaggaaaaataaacg
SEQ ID NO:332	attgttcctttctaaatattctacc
SEQ ID NO:333	cagcacttggaggctgagg
SEQ ID NO:334	cacagaggttcacagtgcgg
SEQ ID NO:335	aacttctgcctgtccataatgc
SEQ ID NO:336	gcctgtaatcccaggactttgg

54

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:337	gccagtaaacatatgaaaagggtgc
SEQ ID NO:338	aattatgttaataaagagtgaaaagg
SEQ ID NO:339	ccccatcacagaaaaacaattcc
SEQ ID NO:340	tgagtgtcaaagaaaaatacaattgg
SEQ ID NO:341	atacacagagaaaaatgagtcacc
SEQ ID NO:342	aacactcccttctgttttagc
SEQ ID NO:343	gatattttgcacacctaggatgc
SEQ ID NO:344	ctctaaaactaatcagcaatgtacc
SEQ ID NO:345	cacctgtatcccgacactttgg
SEQ ID NO:346	cgtaaaactgccacaaagctttagg
SEQ ID NO:347	gtggcagaggtgcagcaagc
SEQ ID NO:348	acagaaaatgacaaacgcatttacc
SEQ ID NO:349	acactcttttagctaggctttgg
SEQ ID NO:350	gagcttggaatagggcagttcc
SEQ ID NO:351	ctgggttctttaacatgtccagg
SEQ ID NO:352	tcaagaaaggacactgcagttgc
SEQ ID NO:353	catgcacacaaactatctcattcc
SEQ ID NO:354	tagccggcatggcgcacg
SEQ ID NO:355	atcatgtgattgaattcaaatacg
SEQ ID NO:356	ttggcgtcaggcagtgacc
SEQ ID NO:357	ggtgttgcagataataacacctgc
SEQ ID NO:358	ttgctatataataatcattgtatcc
SEQ ID NO:359	cggtaactgttactctggatgg
SEQ ID NO:360	aggcttagttccctctttcc
SEQ ID NO:361	gtagtgccttagcacagaaaaagc
SEQ ID NO:362	ctagcctggcaacaagagcg
SEQ ID NO:363	tctctctctctgtggatcg
SEQ ID NO:364	gtttgaatattttgtatgcagcaagc
SEQ ID NO:365	tagaacaattctggcttataaaagc
SEQ ID NO:366	ccactctacccatttgc
SEQ ID NO:367	agaccagaatatgcacagg
SEQ ID NO:368	ggacgtttgcgtgtcg
SEQ ID NO:369	aaggaaacaaactgtgtcacatgc
SEQ ID NO:370	atgttagctggactacagggtgc
SEQ ID NO:371	ggctcatgcctgtatcccagc
SEQ ID NO:372	atgaggtttcacacaaaaagatgc
SEQ ID NO:373	tgggcgcacagagcaagactcc
SEQ ID NO:374	aaatgtccctaaaagtgtacacagc
SEQ ID NO:375	cagactcagtttacctcatcgc

55

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:376	agtgatcttcctctttaacctcc
SEQ ID NO:377	ccagctattcaggaggccaagg
SEQ ID NO:378	cttaaacattatgacactgtctgc
SEQ ID NO:379	ccaggtctatgaggecgttcc
SEQ ID NO:380	tccaaaggcatccctacattatacc
SEQ ID NO:381	acatacacatcatgcagtgactgc
SEQ ID NO:382	tacaggtgccagccaccatgc
SEQ ID NO:383	gcctgtaatcccagcactctgg
SEQ ID NO:384	gacagagtcccactcttgttgc
SEQ ID NO:385	gtgcctccaaagcagtgttagg
SEQ ID NO:386	tatcttaactgggtatgtataatgcc
SEQ ID NO:387	caaaggaaatacgtcttaccagg
SEQ ID NO:388	cctttctcacagacatgcttcc
SEQ ID NO:389	taaacacagtgagcagaatccc
SEQ ID NO:390	ataaagcaaactctaaaagggtcc
SEQ ID NO:391	accactacactccagcctggg
SEQ ID NO:392	gatacctgggtcagagaatgtc
SEQ ID NO:393	tgtatatctcagacttgggagg
SEQ ID NO:394	gtgtcgtcttcttcttcttacg
SEQ ID NO:395	ctggctagtagttaggttggtgc
SEQ ID NO:396	ggactagccacattcaaccagg
SEQ ID NO:397	gcagtatactgagaatttagttcc
SEQ ID NO:398	gaggctgaggcaggagaatgg
SEQ ID NO:399	cattgtttagtgaaggtaacagc
SEQ ID NO:400	cagacaagagtggctacggcag
SEQ ID NO:401	acgcccagccagattattcagg
SEQ ID NO:402	ggaaccagaaagaagtgc当地
SEQ ID NO:403	tgagccatctggaggcaggc
SEQ ID NO:404	caggaccttcttacaaacctcc
SEQ ID NO:405	aacacaacatatctgacccatgc
SEQ ID NO:406	gccttagaagtccagaggaaagc
SEQ ID NO:407	tgacgtacccagtagacccttc
SEQ ID NO:408	ctctgcaaggctggaaacagg
SEQ ID NO:409	gccttgtcccaagtcctaagg
SEQ ID NO:410	gcaaaggactccttggaaattcc
SEQ ID NO:411	gctcctgcctgtatcccagc
SEQ ID NO:412	gaaggaaacagaaaaagcagaggc
SEQ ID NO:413	cttactaccgtttcttcttactgg
SEQ ID NO:414	actattctgtttctttagttactgc

56

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:415	cggtggctcacacctgtaatcc
SEQ ID NO:416	agccagagttctgtgtcttagg
SEQ ID NO:417	taatttgcatttcgtgcgcgtcc
SEQ ID NO:418	cacttttaatacagatccaaatagg
SEQ ID NO:419	atgtatTTTCTTGTCAAGC
SEQ ID NO:420	aaatgttaacatttctccctaagg
SEQ ID NO:421	catatgcccagatccccgtctcc
SEQ ID NO:422	acaggtgtgagccgctgcacc
SEQ ID NO:423	gccaagacgtttacagtttggc
SEQ ID NO:424	aggaaaactctgaggatgtggg
SEQ ID NO:425	gtcttatagggcagtctgaattcc
SEQ ID NO:426	ttagaataaaagttagtctcgagg
SEQ ID NO:427	taatttcttcagtttatccctcag
SEQ ID NO:428	cacatgactaattcttattcattcc
SEQ ID NO:429	aaagacctcaagaaaagagtccacc
SEQ ID NO:430	gaccctaaagattatatgcccag
SEQ ID NO:431	aaagtactaatgcagttgtcagc
SEQ ID NO:432	gaggttctcgattccctgc
SEQ ID NO:433	ggagagcagaggaatttacagg
SEQ ID NO:434	agtaatttagaaactgattctaaagacg
SEQ ID NO:435	cataccattgccaatccagttcc
SEQ ID NO:436	attacgggtgcctgcccactgc
SEQ ID NO:437	cagccaggcagaggagagagg
SEQ ID NO:438	ttttcattccaaagtttctgtttgg
SEQ ID NO:439	tttccaaataggaatttggataatccc
SEQ ID NO:440	taagccagatcacaccactgc
SEQ ID NO:441	ccttcagcgcattatatcttggc
SEQ ID NO:442	ccatctaattccatcttaattcacc
SEQ ID NO:443	gagtggagactgcgcactgc
SEQ ID NO:444	aatcatgtgccaattaaaccatggc
SEQ ID NO:445	cccaggaccagaccagacc
SEQ ID NO:446	ctcaactaccaggatggaaatcagc
SEQ ID NO:447	ggttgcctcgactctgacc
SEQ ID NO:448	gttccccagctcccttctgc
SEQ ID NO:449	agaaagatgtagaagggtccagg
SEQ ID NO:450	ggggaaaagggtgtattatgc当地
SEQ ID NO:451	ctctctcagacctaattgc当地
SEQ ID NO:452	aactatacacatgc当地
SEQ ID NO:453	aaattaatgc当地

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:454	ctttctccactciaagagaaccc
SEQ ID NO:455	tttggtgtgttcattggctgc
SEQ ID NO:456	gcttccacaatgacagacaaaagg
SEQ ID NO:457	ggctcatgtgttaatcccagc
SEQ ID NO:458	catatgaattgtgttccctttagg
SEQ ID NO:459	cactggtacaagtccaagagtcc
SEQ ID NO:460	gaccctgtgtctacttccctggg
SEQ ID NO:461	tatttgaactatcttgcattgtcc
SEQ ID NO:462	ctgattaaaaaggattacccttggc
SEQ ID NO:463	tttggaaactgcactcaataacttgg
SEQ ID NO:464	agtaatgtgtcatgttgcattggc
SEQ ID NO:465	gaaagcattcccaatgtctcacc
SEQ ID NO:466	caatggacaaaaggcccaactgc
SEQ ID NO:467	tccagctctggctttttgttaag
SEQ ID NO:468	acggagtctcactccgtgacc
SEQ ID NO:469	ctatgtcatagtcagagactttgc
SEQ ID NO:470	gttcaaggcattctctgtctcg
SEQ ID NO:471	ccacctaatacttaatacggaaac
SEQ ID NO:472	atattcaacaaacttaatgtgaagtg
SEQ ID NO:473	ttacaggcgtgagtcaccatgc
SEQ ID NO:474	aacaccttcaagaggccaaacg
SEQ ID NO:475	tactattggcaaatttcaatttatgg
SEQ ID NO:476	agccccacatecttaaaattcaataag
SEQ ID NO:477	gaaagtggataagtgtttgtctgg
SEQ ID NO:478	ggccaggcattcaagaccagc
SEQ ID NO:479	agccaaacaacaaaaagacacaacc
SEQ ID NO:480	ttgagcccaggagttcaagacc
SEQ ID NO:481	cagactaaagatctcagagaaaaac
SEQ ID NO:482	cgcttgcataatcccgacttgg
SEQ ID NO:483	aaaagtgaaatcagaattttttcc
SEQ ID NO:484	caggcgtgagcaactgtgtcc
SEQ ID NO:485	ggtccagtaggatctcggttgc
SEQ ID NO:486	actttgaaaatgtgttatacgctgg
SEQ ID NO:487	ttccctgcatacttgcattttcc
SEQ ID NO:488	agatatctaccattgaagagttgc
SEQ ID NO:489	agtcttcaacttacttgcattttcc
SEQ ID NO:490	ccatgcaggatgaaaataaaaagc
SEQ ID NO:491	tgggtgacagagttgagactcc
SEQ ID NO:492	acagcaataccgggttaacatgc

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:493	tttatgtaaaagatgaatgcgaggc
SEQ ID NO:494	ctactctgtactggaaacagg
SEQ ID NO:495	caaacgttagtctggcaaaatgcg
SEQ ID NO:496	tgcacgttacccacacccaggc
SEQ ID NO:497	aattcttggatctgtgttactgc
SEQ ID NO:498	taccagttatcattctctttctgc
SEQ ID NO:499	atccacccacctcggcctcc
SEQ ID NO:500	cactctgcctggcccttaatgg
SEQ ID NO:501	atagtttggtaatatgccactaagg
SEQ ID NO:502	gctgtgagccacccgacccctgg
SEQ ID NO:503	ctccatcacacaatttatgtggc
SEQ ID NO:504	agacggagtctcggttgc
SEQ ID NO:505	tcccaggttcaagccatttc
SEQ ID NO:506	tattttgagagtctcactctgtcg
SEQ ID NO:507	gtctcgaactcctgaccctcagg
SEQ ID NO:508	aaggagggtgaagagtgaactacg
SEQ ID NO:509	gtctcagggtttggacttacttgg
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SEQ ID NO:511	gtacactgaacaaaggagacagg
SEQ ID NO:512	ctggtagataatgcacaaatagcacc
SEQ ID NO:513	catttaatgtgaaatgaattataagcc
SEQ ID NO:514	gagacagggtttcaactatgttgg
SEQ ID NO:515	ccagcacttggaaaggctgagg
SEQ ID NO:516	gaaaccaagtatcatggtaattgc
SEQ ID NO:517	cagtggggctgtcagttcc
SEQ ID NO:518	gccagggtcggtggctc
SEQ ID NO:519	catgcctgtaatcccagctacc
SEQ ID NO:520	atgtaaaatggtagcactttagg
SEQ ID NO:521	cccacaatacagagaactcttacc
SEQ ID NO:522	tgaaacatgcagcccccagtgcc
SEQ ID NO:523	tgtttttctccgtcctcaatcc
SEQ ID NO:524	gttttccctgggtctccatctgg
SEQ ID NO:525	gcagccgcttggaaaacaaaacagc
SEQ ID NO:526	gtacacgttacattttgggggtgg
SEQ ID NO:527	taggctggaaaactaaaattttgtgc
SEQ ID NO:528	ctcccttgggtctccatctgg
SEQ ID NO:529	gcctcggtctccaaagtgc
SEQ ID NO:530	aatgcctagagagatttggcagg
SEQ ID NO:531	gagatggggtttcaactatgttgg

**59**

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:532	tgtgatcttgcactgcactcc
SEQ ID NO:533	acttctcctccattgtttttcg
SEQ ID NO:534	cgtccccgggctcagttctac
SEQ ID NO:535	ccaaaacaataaaatcacaatttggg
SEQ ID NO:536	ctgaactgccttagttaaatccg
SEQ ID NO:537	atttctgtatcagggtctgtttcc
SEQ ID NO:538	ggctgacccttcactgtttcc
SEQ ID NO:539	caaaaattagccaggcatggtgg
SEQ ID NO:540	gcagtgagcagtgtatgcacc
SEQ ID NO:541	aaagactgtgaactaacttgttgc
SEQ ID NO:542	tgccaagaattacacattatttaggc
SEQ ID NO:543	ggccaggatgtcattaactttcc
SEQ ID NO:544	gttaagagctgacgtgtattgtgc
SEQ ID NO:545	cccggtgaggccgcacatcc
SEQ ID NO:546	cctgcgccttaaaaaacccctcc
SEQ ID NO:547	cggcgcttagggccatcg
SEQ ID NO:548	acttaaggaaacgaacatgacacc
SEQ ID NO:549	gagaccgagtcgtgtgtcg
SEQ ID NO:550	gtattaaattgaagatgatggatgc
SEQ ID NO:551	tctttaaaagactatcgctgaggc
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SEQ ID NO:553	gttcatgtttcttgcgtctcc
SEQ ID NO:554	tttcgaaagttcaggctgagtgc
SEQ ID NO:555	gaccctcaaaacaatcctctaagg
SEQ ID NO:556	caaaacacacttagaaacaaactgc
SEQ ID NO:557	gcctggcgacatagtgagacc
SEQ ID NO:558	ggcaggagaatggcgtgaacc
SEQ ID NO:559	tttgctcggttgcggcgttgg
SEQ ID NO:560	gcaacttaatgtatagaataatagc
SEQ ID NO:561	cctcccccctgtctgccage
SEQ ID NO:562	ccacaacaatgtaaactcctctgg
SEQ ID NO:563	tactctcccttagagttcggttccc
SEQ ID NO:564	gggtccccctttggccattcc
SEQ ID NO:565	gatcttggctcaattcaacctcc
SEQ ID NO:566	agggaaatattaaaccccttgg
SEQ ID NO:567	aatgcaatggtgcatcacagagg
SEQ ID NO:568	tcatttatctatttctacatggtcc
SEQ ID NO:569	ggaaggaaatgcccgtgaacc
SEQ ID NO:570	agtgaacatttctgcagcctcc

**60**

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:571	caacaggacgtcaggcgatcc
SEQ ID NO:572	ccttcaggctgtcctgaaaagg
SEQ ID NO:573	agtctcactccatgcggcagg
SEQ ID NO:574	actgtgaacagtagttaactagg
SEQ ID NO:575	gcatgcctgtatccaagctgc
SEQ ID NO:576	gaaacaattctctttcacacttgc
SEQ ID NO:577	ggctcatgcctgttatccagc
SEQ ID NO:578	agaagaagcttagtcatatgtttgg
SEQ ID NO:579	cagatgtttagccaaacaaatgg
SEQ ID NO:580	ctggcagacagagtgagactcc
SEQ ID NO:581	aatgtgtgaatattattcattacaggg
SEQ ID NO:582	gcaggagaattgtgttgcacctgg
SEQ ID NO:583	cttttagtcaaattaaaacagtctatcc
SEQ ID NO:584	gatttctatctcctgcaccacc
SEQ ID NO:585	ttcttggtactactaaaaatctcc
SEQ ID NO:586	aaagggtcttcataaggctaatgg
SEQ ID NO:587	ctcttaaggattatttatatgaagacc
SEQ ID NO:588	caggaggagccccagagc
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SEQ ID NO:591	agtcaaggcaggctctgcc
SEQ ID NO:592	tattttggccccatccagaaagc
SEQ ID NO:593	cacccagagttacagttgttcc
SEQ ID NO:594	gaggaggccccagacgcctgc
SEQ ID NO:595	tggggatgggttgcattacc
SEQ ID NO:596	cccacagagttacacagctgc
SEQ ID NO:597	caggctctcccactcacc
SEQ ID NO:598	ccatccagaaagccccaaagcc
SEQ ID NO:599	ccagagttacagttgttcccttattc
SEQ ID NO:600	gcagtacaaacaacgcacagcg
SEQ ID NO:601	ctgccacccctccacagtccc
SEQ ID NO:602	gccaagaccatgcacgc
SEQ ID NO:603	cccaggacaaaagagactccc
SEQ ID NO:604	caggaagcagacagtcttcttagttcc
SEQ ID NO:605	tgcctgtatccaaacactttgg
SEQ ID NO:606	tccctctggccaggatgggg
SEQ ID NO:607	atggggatgggatggagtaggaagc
SEQ ID NO:608	cagatcagttctccctccagc
SEQ ID NO:609	acaaaaaaaaagaaacatgcagagagg

## US 9,145,587 B2

**61**

TABLE 1-continued

Sequence Identifier	Sequence
SEQ ID NO:610	tggtggcatgcatctgttagtcc
SEQ ID NO:611	aggtgctctatacgatgttagcatccc
SEQ ID NO:612	ccaggacaggatggagatctgg
SEQ ID NO:613	agggAACCTGTGCATTATCCTTG
SEQ ID NO:614	cagaagtcttgcttaaggaggagg
SEQ ID NO:615	gggtacgtgaaactcaccaagg
SEQ ID NO:616	cagagtgtggcaagcaagg
SEQ ID NO:617	aacattttaaaggtacaataacgtgg
SEQ ID NO:618	tagggagcaacagccatta
SEQ ID NO:619	ggtcactgtccagctctgg
SEQ ID NO:620	actctcgctgaaactcgctgg
SEQ ID NO:621	ctcggtctctggtagtacgc
SEQ ID NO:622	gcaagagggtccgagctggg

**62**

TABLE 1-continued

Sequence Identifier	Sequence
5	SEQ ID NO:623
	ggaagaagtgaaacaagagatgaagg
	SEQ ID NO:624
	cccagagaacaaaccggattagg
	SEQ ID NO:625
	cccttcaaccccttccaatctgc
10	SEQ ID NO:626
	ccatgtccagtgggttaggg
	SEQ ID NO:627
	gagattggtagggagacagatgg
	SEQ ID NO:628
	cttctcagctcaaagtccagcg
15	SEQ ID NO:629
	gaatggagagatgaccagagg
	SEQ ID NO:630
	aaggcaagggggtatgtgg
	SEQ ID NO:631
	ggaaggaagcatggaaacacc
20	SEQ ID NO:632
	ccatcaatgctgtctgtctgg
	SEQ ID NO:633
	gtgccgtactgtgcttgg
	SEQ ID NO:634
	acatcccattgacctcatcaagc

## SEQUENCE LISTING

&lt;160&gt; NUMBER OF SEQ ID NOS: 634

<210> SEQ ID NO 1  
<211> LENGTH: 203  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: BCR region

&lt;400&gt; SEQUENCE: 1

gtggggccccc ccgtttccgt gtacaggcga cctgcagggaa gggcaggcag ctgcctgaa	60
ggctgatccc cccttcctgt tagcactttt gatggacta gtggactttg ttcaagg	120
aagagctatg cttgttaggg cttcttgct cttccagga gtggacaagg tgggttagga	180
gcagtttctc cctgagtggc tgc	203

<210> SEQ ID NO 2  
<211> LENGTH: 376  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: ABL region

&lt;400&gt; SEQUENCE: 2

caccacgtct ggctaatttt tttttttt gtagagatgg gtttcaaca tgtagccag	60
gttgtctcg aactcctgac ctcaggtgtat ccacccgct gggccctcca aagtgtgg	120
attacaggca ggagccactg tgcccgct gacccatata ttgaataccg agtttagtt	180
ctggaggagc tgcagggttt atgaaaaggg aacacatgg atccctcaga gcagccacag	240
gccagctctc tgaagtaaaag tgcacgtgtg catgtgtgtg cacactcaca cacacgtaca	300
cacacattca caaataactg tgcccgct gacccatata ttgaataccg agtttagtt	360
ctggaggagc tgcagg	376

<210> SEQ ID NO 3  
<211> LENGTH: 231

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<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: BCR region

<400> SEQUENCE: 3

tttggggc tgaggcaggt ggatcgcttg agtcaggag ttggagacca gcctgaccaa	60
catggtaaaa ccctgtgtct actaaaaata caaagattag cccggctagg cagtggcac	120
ctgtaatcac aactgcgttgg gaggctgagg gaagagaatc gcttgaaccc aggaggcgga	180
ggttgcagtg agccgagctt gtgccactgc attccagect gggcgacaga g	231

<210> SEQ ID NO 4  
<211> LENGTH: 249  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: ABL region

<400> SEQUENCE: 4

ggtctcaactc ttttgaactc ctgggtggcct caagggatcc tcc tacactcg gcctcacaaa	60
gtatttggaa tacagggtgtg agtcaactgca gctggccttc acttataact gtgaggagta	120
aacagctgca tgggtggcctt aatgccatct aacacgagtg actccatgtt cagacagtag	180
gatcacaat gattattata tagcaatgaa tggccacagg tacatagact aaggagccac	240
atccctgtct	249

<210> SEQ ID NO 5  
<211> LENGTH: 212  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: BCR region

<400> SEQUENCE: 5

cctccagcta cctgecagcc ggcacttttgc tcaaggctgt tttgcattca ctgtgcaca	60
tatgctca gtcacacacaca gcatacgcta tgcacatgtt tccacacaca ccccaccac	120
atccccacatc accccgaccc cctctgtgtt ctttggaaacc ttattacact tcgagtca	180
ggtttgcctt tattgtgaaa ccagctggat cc	212

<210> SEQ ID NO 6  
<211> LENGTH: 200  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: ABL region

<400> SEQUENCE: 6

ttattttataa caacattttc agcgtggcaa ctgcagtttca agaatggtttgg aattatacca	60
gtcagagaga gatgcaaattt atttaaaata ggaagaaagc aggtgtctgg cccagaggac	120
cagattaaga agaccccatg agagttacaa tagtttgttga aaatgggtct tctgcaaacc	180
tcatgtotac agaagctgg	200

<210> SEQ ID NO 7  
<211> LENGTH: 213  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: BCR region

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<400> SEQUENCE: 7

```
tgcacacctca taacataatc tttctcctgg gcccctgtct ctggctgcct cataaacgct      60
gggttccccc tcgtgggcct ccctgcattcc ctgcatttc tcccggtcc tgtctgttag      120
caatacagcg tgacacccta cgctgccccg tggcccccggg cttgtcttc cttgccc      180
tggtaacctt ctttcttatct cttcccttgcg ccg                                213
```

<210> SEQ ID NO 8  
<211> LENGTH: 251  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens  
<220> FEATURE:  
<223> OTHER INFORMATION: ABL region

<400> SEQUENCE: 8

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gtgagctccg cctccgtca gatcagtggc ggcattagtt tctcatagga gcatgaaatc      60
tattgtgaac agtacatgcg atggatccag gttgcgtgct cctagtgaga atctaatgcc      120
tgaggatctc tcattgtctc ttatcactcc cagataggac tgtctagttg caggaaaca      180
agctcagggc tcccactgtat tctacattac agtgggttg ataattatata tatattacaa      240
tgtaataata a                                         251
```

<210> SEQ ID NO 9  
<211> LENGTH: 63  
<212> TYPE: DNA  
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

```
ggagtctgag gaggggaagg aggcaagggtt ggctcggatc ccagccagta agtctgggtg      60
tgg                                         63
```

<210> SEQ ID NO 10  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 10

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cttcccttg acatccgtgg                                         20
```

<210> SEQ ID NO 11  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 11

```
acacagcata cgctatgcac atgtg                                         25
```

<210> SEQ ID NO 12  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 12

```
gagggttgttcc agatgaccac gg                                         22
```

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<210> SEQ ID NO 13  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 13  
  
cagctactgg agctgtcaga acag

24

<210> SEQ ID NO 14  
<211> LENGTH: 17  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 14  
  
tgggcctccc tgcattcc

17

<210> SEQ ID NO 15  
<211> LENGTH: 17  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 15  
  
tccccctgca ccccacg

17

<210> SEQ ID NO 16  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 16  
  
tgacatccgt ggagctgcag atgc

24

<210> SEQ ID NO 17  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 17  
  
acatgtgtcc acacacaccc cacc

24

<210> SEQ ID NO 18  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
  
<400> SEQUENCE: 18  
  
accacacggac acctttgacc ctgg

24

<210> SEQ ID NO 19  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 19

ctggagctgt cagaacagt g aagg

24

&lt;210&gt; SEQ ID NO 20

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 20

tccctgcata cctgcata tc tcc

24

&lt;210&gt; SEQ ID NO 21

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 21

cccacgactt ctccagcact g a g c

24

&lt;210&gt; SEQ ID NO 22

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 22

gcaacactgt gacgtactgg agg

23

&lt;210&gt; SEQ ID NO 23

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 23

gtctatctaa aattcacaag gaatgc

26

&lt;210&gt; SEQ ID NO 24

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 24

aggcaaagta aaatccaagc accc

24

&lt;210&gt; SEQ ID NO 25

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 25

cactcctgca ctccagcctg g

21

&lt;210&gt; SEQ ID NO 26

&lt;211&gt; LENGTH: 24

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 26

caaccaccaa agtgctttc ctgg

24

<210> SEQ ID NO 27  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 27

atatggcatc tgtaaatatt accacc

26

<210> SEQ ID NO 28  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 28

tgcctcgccc tcccaaagtg c

21

<210> SEQ ID NO 29  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 29

agccaccaca cccagccagg

20

<210> SEQ ID NO 30  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 30

aataactgtt ttctcccccc aaaac

25

<210> SEQ ID NO 31  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 31

tgttttacaa aaatggggcc atacc

25

<210> SEQ ID NO 32  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 32

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acttaagcaa attctttcat aaaaaggg	28
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<210> SEQ ID NO 33  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 33  
cttcaattt ttgtaccaac tctcc

25

<210> SEQ ID NO 34  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 34  
acctcctgca tctctccctt tgc

23

<210> SEQ ID NO 35  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 35  
aaataaaagg ttgagaacca taagtgg

27

<210> SEQ ID NO 36  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 36  
caccatcaca gtcactgca gc

22

<210> SEQ ID NO 37  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 37  
aaccttttg agaatcgat agcc

24

<210> SEQ ID NO 38  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 38  
aaataaaagta catacctcca attttgc

27

<210> SEQ ID NO 39  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 39  
gacacattcc tatgggttta attcc 25

<210> SEQ ID NO 40  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 40  
tgtaaaatat ggtttcagaa gggagg 26

<210> SEQ ID NO 41  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 41  
gcagggtggat aacgagggtca gg 22

<210> SEQ ID NO 42  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 42  
ccagccaaga atttcaaaga ttagc 25

<210> SEQ ID NO 43  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 43  
gaagggagat gacaaaggga acg 23

<210> SEQ ID NO 44  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 44  
gcagaagaac tgcttgaacc tgg 23

<210> SEQ ID NO 45  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 45  
gtggtcccag ctactcgaga gg 22

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<210> SEQ ID NO 46  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 46

ccctcagcaa aactaactga aaagg

25

<210> SEQ ID NO 47  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 47

tagaaaccaa gatatctaga attccc

26

<210> SEQ ID NO 48  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 48

ccacgccccg cggaataaat gc

22

<210> SEQ ID NO 49  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 49

acaaaaaaaag aggcaaaaac tgagag

26

<210> SEQ ID NO 50  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 50

ctgggcgcag tggctcatgc c

21

<210> SEQ ID NO 51  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 51

tggctgtgag gctgagaact gc

22

<210> SEQ ID NO 52  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 52

ctggggcaca gagtgagact cc

22

&lt;210&gt; SEQ ID NO 53

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 53

aagtctggct gggcgcatgt g

21

&lt;210&gt; SEQ ID NO 54

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 54

aatggacaaa agaggtgaac tggc

24

&lt;210&gt; SEQ ID NO 55

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 55

gatagagtga aaacgcacaa tggc

24

&lt;210&gt; SEQ ID NO 56

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 56

aattaaacag ctaggtcaat atgagg

26

&lt;210&gt; SEQ ID NO 57

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 57

ggtctccact atcaaggac aag

23

&lt;210&gt; SEQ ID NO 58

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 58

aagcagctgt tagtcatttc cagg

24

&lt;210&gt; SEQ ID NO 59

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<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 59

aggcatcctc agattatggc tcc

23

<210> SEQ ID NO 60  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 60

cctgagtaac actgagaccc tgc

23

<210> SEQ ID NO 61  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 61

aacactcaag ctgtcaagag acac

24

<210> SEQ ID NO 62  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 62

attcaggcca ggcgcagtgg c

21

<210> SEQ ID NO 63  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 63

taaatcgtaa aactgccaca aagc

24

<210> SEQ ID NO 64  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 64

cagaggagta ggagaaggaa aagg

24

<210> SEQ ID NO 65  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 65

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ggtagctatc taccaagtag aatcc 25

<210> SEQ ID NO 66  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 66

atcagattgg aaaaagtccc aaagc 25

<210> SEQ ID NO 67  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 67

ctcctgaaaa gcacctaactc agc 23

<210> SEQ ID NO 68  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 68

tcgccttaaac ctgaggtaact ggg 23

<210> SEQ ID NO 69  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 69

ttttctcccta atagaccacc attcc 25

<210> SEQ ID NO 70  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 70

ctgctgtatt accatcaactc atgtc 25

<210> SEQ ID NO 71  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 71

ctggccaaca tagtgaacc acg 23

<210> SEQ ID NO 72  
<211> LENGTH: 27  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 72  
atttgaatag gggtaaagt atcattg 27

<210> SEQ ID NO 73  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 73  
cacttcagtg gaagttggca tgc 23

<210> SEQ ID NO 74  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 74  
gtttttcttc gaagtataaa acatacg 27

<210> SEQ ID NO 75  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 75  
gctccttagt ctatgtacct gtgg 24

<210> SEQ ID NO 76  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 76  
tactctggca tggtaactgg tgc 23

<210> SEQ ID NO 77  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 77  
acaaaggact aggtctgtgg agc 23

<210> SEQ ID NO 78  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 78  
ccaaaggacttac caaattacca aagttacc 28

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<210> SEQ ID NO 79  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 79

tgagccgata tcacgccact gc

22

<210> SEQ ID NO 80  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 80

tcccaataaa gggtttggcc cagg

24

<210> SEQ ID NO 81  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 81

ctgggttagca aatttagggaa cagg

24

<210> SEQ ID NO 82  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 82

ctggccagaa aagacagttt tatcc

25

<210> SEQ ID NO 83  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 83

ggttcccagg aaggataaac acc

23

<210> SEQ ID NO 84  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 84

tcactccagg aggttccatt tcc

23

<210> SEQ ID NO 85  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 85

aggcttggaa ataaggcagca gtgg

24

&lt;210&gt; SEQ ID NO 86

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 86

attcatacaa tggaaatacta ctcagc

26

&lt;210&gt; SEQ ID NO 87

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 87

taagtgtatcc tccccaccta acc

23

&lt;210&gt; SEQ ID NO 88

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 88

tataagagga agactggggc tgg

23

&lt;210&gt; SEQ ID NO 89

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 89

tcataacttat gcaggttata ggagg

25

&lt;210&gt; SEQ ID NO 90

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 90

caagatcacg ccactgcact cc

22

&lt;210&gt; SEQ ID NO 91

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 91

aaaataaataa gctgggtgctc aagatc

26

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<210> SEQ ID NO 92  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 92

caccaggctc attcaacaga tgg

23

<210> SEQ ID NO 93  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 93

caatgcagcc tcaacccctt gg

22

<210> SEQ ID NO 94  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 94

gttaggtcag gtgctcatgt ctg

23

<210> SEQ ID NO 95  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 95

aagtttcaa aggacatgtt caaaaatg

27

<210> SEQ ID NO 96  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 96

tcctgaagag gctgcagtt cc

22

<210> SEQ ID NO 97  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 97

ctgggtgcaca ttcccaagtg tgc

23

<210> SEQ ID NO 98  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 98

catgttggcc atgttcttct gagg

24

<210> SEQ ID NO 99  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 99

ctcagcctcc cgagtagctg g

21

<210> SEQ ID NO 100  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 100

aaagacattt aagaggagat gaggc

25

<210> SEQ ID NO 101  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 101

tgctgggatt acaggcgtga gc

22

<210> SEQ ID NO 102  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 102

tgtgacttcc atcccgagct cc

22

<210> SEQ ID NO 103  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 103

gacacttttg tggagcttcc atgg

24

<210> SEQ ID NO 104  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 104

catgtgaggg ggcacgtctt gc

22

<210> SEQ ID NO 105  
<211> LENGTH: 25

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 105

tcttcttat gagaaaagtg gttgc

25

<210> SEQ ID NO 106  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 106

tggcaaaatg ctatcgagct gcc

23

<210> SEQ ID NO 107  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 107

tatgaacaca gccggcctca gg

22

<210> SEQ ID NO 108  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 108

gagggttcag tgagctgaga tcg

23

<210> SEQ ID NO 109  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 109

gtcaaggcacc cagtccgata cc

22

<210> SEQ ID NO 110  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 110

atctgggctt ggtggcgcac g

21

<210> SEQ ID NO 111  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 111

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gttaagcggg tccccatca gc 22

<210> SEQ ID NO 112  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 112  
cagccagttt cagtagaaag atgc 24

<210> SEQ ID NO 113  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 113  
gacccaagca taagggact agc 23

<210> SEQ ID NO 114  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 114  
cccaaaaagt ttacaagaga aattttc 27

<210> SEQ ID NO 115  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 115  
cgccctgttgtt cccagctact cg 22

<210> SEQ ID NO 116  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 116  
cgcggtatgc ggaaaaagaaa tcc 23

<210> SEQ ID NO 117  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 117  
tctactatga accctccatca agac 24

<210> SEQ ID NO 118  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 118

gtgctggat tacaggtgt agc

23

<210> SEQ ID NO 119  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 119

ttatccaaat gtcccaggc agg

23

<210> SEQ ID NO 120  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 120

ctgccagcac tgctcgccag c

21

<210> SEQ ID NO 121  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 121

gctactgcag gcagtgcctt cc

22

<210> SEQ ID NO 122  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 122

catccaagcc caaggtgtca gg

22

<210> SEQ ID NO 123  
 <211> LENGTH: 25  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 123

tgttgtcatg taatttcagg aagcc

25

<210> SEQ ID NO 124  
 <211> LENGTH: 24  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 124

gatccgtcac tgttaacact cagg

24

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<210> SEQ ID NO 125  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 125

ctcacagtca caagtcctg agc

23

<210> SEQ ID NO 126  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 126

gagatgtatgc tgggttcaca gg

22

<210> SEQ ID NO 127  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 127

ttagaagaat gggatcgcaa agg

23

<210> SEQ ID NO 128  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 128

cggatttcaa atatgaggc aggc

24

<210> SEQ ID NO 129  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 129

gttaaatccctg ctgccagtct tcc

23

<210> SEQ ID NO 130  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 130

acagggtcag acagagcctt gg

22

<210> SEQ ID NO 131  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 131

agtattatggat ctaactatac aacaaggc

27

<210> SEQ ID NO 132  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 132

aaagactagg ggccggggac g

21

<210> SEQ ID NO 133  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 133

ctggtagaaa taaagacaac aaagcc

26

<210> SEQ ID NO 134  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 134

gtgccaagta attaaaaagtt tgaaacc

27

<210> SEQ ID NO 135  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 135

ggctttgaa gggagcacca cc

22

<210> SEQ ID NO 136  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 136

gaaggataaa tacctatgat actttcc

27

<210> SEQ ID NO 137  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 137

ggcaggaaaa tactgtgctt caag

24

&lt;210&gt; SEQ ID NO 138

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<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 138

gtggtgaaat tccacacctag tacc

24

<210> SEQ ID NO 139  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 139

tcccaaagtgc tgggattac agg

23

<210> SEQ ID NO 140  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 140

gaaatttagca aacaatgcc a gacg

25

<210> SEQ ID NO 141  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 141

taagtattgg accggaaagg agg

23

<210> SEQ ID NO 142  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 142

ctatcatttt gctcaaagtgc tagcc

25

<210> SEQ ID NO 143  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 143

atttcacaaa ctacagaggc cagg

24

<210> SEQ ID NO 144  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 144

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tagacttctg tctcttatg ctgc 24

<210> SEQ ID NO 145  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 145

tgagtggact gccatgtat acc 23

<210> SEQ ID NO 146  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 146

acttcacacc agcctgtcca cc 22

<210> SEQ ID NO 147  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 147

taactcatat cctcagagag accc 24

<210> SEQ ID NO 148  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 148

agagggttcct cgattccct gc 22

<210> SEQ ID NO 149  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 149

gtgtcagcgt cccaaacacaa agc 23

<210> SEQ ID NO 150  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 150

gaaaagtggat gggcaagcat tgc 23

<210> SEQ ID NO 151  
<211> LENGTH: 22  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 151

gtgatcacct cacagctgca gg

22

<210> SEQ ID NO 152  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 152

gttggttag tcaaggcatt tcacc

25

<210> SEQ ID NO 153  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 153

cctcagcctc cagagtagct gg

22

<210> SEQ ID NO 154  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 154

taaaagaaaa ctccctccttc ctgg

24

<210> SEQ ID NO 155  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 155

aatgtgctat gtcttaaat ccatgg

26

<210> SEQ ID NO 156  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 156

agctggcaaa tctggtaata taaaag

26

<210> SEQ ID NO 157  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 157

gcttgaacct ggaagggtgga gg

22

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<210> SEQ ID NO 158  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 158

gcaggcatgc taagaccc ttca

23

<210> SEQ ID NO 159  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 159

cagctccatg aataactcca cagg

24

<210> SEQ ID NO 160  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 160

gcttgaaccc aggaggcaga gg

22

<210> SEQ ID NO 161  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 161

atcgaagatg ccactgcaag agg

23

<210> SEQ ID NO 162  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 162

ccaaaccacac ttcaggggat acc

23

<210> SEQ ID NO 163  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 163

cacgccatgc cactgatact cac

23

<210> SEQ ID NO 164  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 164

gggtttcacc atgttggcca gg

22

&lt;210&gt; SEQ ID NO 165

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 165

cccaacaaag gctctggcct gg

22

&lt;210&gt; SEQ ID NO 166

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 166

atgacacgacg aggagcttca tcc

23

&lt;210&gt; SEQ ID NO 167

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 167

gcaggctacg agtaaaagga tgg

23

&lt;210&gt; SEQ ID NO 168

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 168

cgggtaaaat cttgcctcct tcc

23

&lt;210&gt; SEQ ID NO 169

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 169

aaacttaaac caatgggttga tgtgg

25

&lt;210&gt; SEQ ID NO 170

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 170

agagactgag gaactgttcc agc

23

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<210> SEQ ID NO 171  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 171

gaaacggtct tggatcactg atcc

24

<210> SEQ ID NO 172  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 172

tgcgcatgat atcttgttgc aggg

24

<210> SEQ ID NO 173  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 173

ggcctccgtt taaaactgttg tgc

23

<210> SEQ ID NO 174  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 174

gaatgctggc ccgacacagt gg

22

<210> SEQ ID NO 175  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 175

tcttggata gaaaagccag ctgg

24

<210> SEQ ID NO 176  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 176

gaaaaagccc aagagccccct gg

22

<210> SEQ ID NO 177  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 177

ttctcccaa atgagccccca agg

23

<210> SEQ ID NO 178  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 178

gtggtagacgt aaacaaaagg tacc

24

<210> SEQ ID NO 179  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 179

gcaaattcca tgtgaatctt attggc

26

<210> SEQ ID NO 180  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 180

cctgatctat ggaacagtgg tgg

23

<210> SEQ ID NO 181  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 181

gttacaaaacg ttgcagtttg caacg

25

<210> SEQ ID NO 182  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 182

gaaccccgtc aacagtgtac acc

23

<210> SEQ ID NO 183  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 183

acaggacctc aaggcaagga gc

22

<210> SEQ ID NO 184  
<211> LENGTH: 27

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 184

catacctaaa atagaaatgt ctatccc

27

<210> SEQ ID NO 185  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 185

gagttgcata tatgttttat aaatccc

27

<210> SEQ ID NO 186  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 186

ttagcccaaca tccataaagt tagc

24

<210> SEQ ID NO 187  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 187

accgcaacct ttgccgcctg g

21

<210> SEQ ID NO 188  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 188

taaatatttt gtatggagtc accacc

26

<210> SEQ ID NO 189  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 189

aaagccagga gaaaaagtta tgagg

25

<210> SEQ ID NO 190  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 190

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tcccaaagtc ccaggattac agg

23

<210> SEQ ID NO 191  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 191

tcactatggc gcatctccga tgg

23

<210> SEQ ID NO 192  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 192

agtccctgg aagtctccga gg

22

<210> SEQ ID NO 193  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 193

aaaataatca cccagccccac atcc

24

<210> SEQ ID NO 194  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 194

acaaaaactac agacacagaa agtgg

25

<210> SEQ ID NO 195  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 195

tttgggaggc tgaggttagt gg

22

<210> SEQ ID NO 196  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 196

aaagacagtg aaacatctat aaggg

25

<210> SEQ ID NO 197  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 197

cattttggga gaccagggca gg

22

<210> SEQ ID NO 198  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 198

gcatgggaca gacacaaagc agc

23

<210> SEQ ID NO 199  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 199

gaataacaaa gagagccggc tgg

23

<210> SEQ ID NO 200  
 <211> LENGTH: 29  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 200

taaacctttt attgaaaatt gtcaaatgg

29

<210> SEQ ID NO 201  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 201

cgcctcagcc tcccaaagtgc

21

<210> SEQ ID NO 202  
 <211> LENGTH: 26  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 202

tacatttagtt ttatagggcc agtagg

26

<210> SEQ ID NO 203  
 <211> LENGTH: 27  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 203

gaaggtttat tcataataaa atgtgcc

27

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<210> SEQ ID NO 204  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 204

ctggcttcgt tggttgagt tgg

23

<210> SEQ ID NO 205  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 205

acagacccatc ctcctaaggaa tgg

23

<210> SEQ ID NO 206  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 206

gctagctttt gtgtgttaaga atgggg

25

<210> SEQ ID NO 207  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 207

ggcctactca cacaatagaa tacc

24

<210> SEQ ID NO 208  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 208

gcaccattgc actccagcct gg

22

<210> SEQ ID NO 209  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 209

gaaatttagga taaagggttgt cacagc

26

<210> SEQ ID NO 210  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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<400> SEQUENCE: 210  
cagaagtgtt caaggtgaaa ctgtc 25

<210> SEQ ID NO 211  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 211  
ctgaatcatg aatgttcta ctctgc 26

<210> SEQ ID NO 212  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 212  
tgtcaacttg actggccat acg 23

<210> SEQ ID NO 213  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 213  
ctcccgata gttggattta tagg 24

<210> SEQ ID NO 214  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 214  
gcttggagtt cttgaaatt cttgg 25

<210> SEQ ID NO 215  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 215  
cctgggtggct ccagtttct acc 23

<210> SEQ ID NO 216  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 216  
aactcctgac ctcatgatcc acc 23

<210> SEQ ID NO 217

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<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 217

gctgggattt caggcatgag cc

22

<210> SEQ ID NO 218  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 218

ttctccctta tccttggtga cattc

25

<210> SEQ ID NO 219  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 219

tcccaaaggct ctgggattac agg

23

<210> SEQ ID NO 220  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 220

gtcataagtc agggaccatc tgc

23

<210> SEQ ID NO 221  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 221

ctgtttcatt gatttccaga ctggc

25

<210> SEQ ID NO 222  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 222

gcaatctcggtt ctcactgcaa gc

22

<210> SEQ ID NO 223  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 223

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gaagaagtga ctatatacaga tctgg 25

<210> SEQ ID NO 224  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 224

ttcaccatgt tggccaggct gg 22

<210> SEQ ID NO 225  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 225

catcaactgaa gatgacaact gagc 24

<210> SEQ ID NO 226  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 226

gtccagcctg ggcgatagag c 21

<210> SEQ ID NO 227  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 227

gaggaaaagtc tttgaagagg aacc 24

<210> SEQ ID NO 228  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 228

ggtagtacactca ccagcagttt tgc 23

<210> SEQ ID NO 229  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 229

gagcaactgg tgtgaataca tatgg 25

<210> SEQ ID NO 230  
<211> LENGTH: 23  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 230

caataacctgg caccacatac acc

23

<210> SEQ ID NO 231  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 231

gggactacag gcatgtgccca cc

22

<210> SEQ ID NO 232  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 232

cggtggctca cgcgtgtaat cc

22

<210> SEQ ID NO 233  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 233

caactgttaa atctctcatg gaaacc

26

<210> SEQ ID NO 234  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 234

gacaaaggat tagaaatgca ccc

23

<210> SEQ ID NO 235  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 235

ggaaaatgttc taaaactgga ttgtgg

26

<210> SEQ ID NO 236  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 236

aataataataa gccagggttg gttagc

25

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<210> SEQ_ID NO 237
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 237
ctggaacact cacacattgc tgg                                23

<210> SEQ_ID NO 238
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 238
ctgggtgaca gagcagact cc                                22

<210> SEQ_ID NO 239
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 239
cccaaatcat ccccgtaaaa catgc                                25

<210> SEQ_ID NO 240
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 240
gaccctgcaa tccaaacact gg                                22

<210> SEQ_ID NO 241
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 241
ctctcaggcc ttcaaaactac acc                                23

<210> SEQ_ID NO 242
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 242
caggaaaggc ctcgctcagt gg                                22

<210> SEQ_ID NO 243
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 243

atctgcaaaa gcagcagagc agg

23

&lt;210&gt; SEQ ID NO 244

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 244

gtacccatga cagacaagt ttagg

25

&lt;210&gt; SEQ ID NO 245

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 245

cttatecccact actgtctcct ttgg

24

&lt;210&gt; SEQ ID NO 246

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 246

ggatggtctc gatccctga cc

22

&lt;210&gt; SEQ ID NO 247

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 247

aggtagaga ctttcctcta atgc

24

&lt;210&gt; SEQ ID NO 248

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 248

agctgggatt acaggtgcct gc

22

&lt;210&gt; SEQ ID NO 249

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 249

gctgaggcag gttggggctg c

21

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<210> SEQ ID NO 250  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 250

acattnaacg tctcctaact tctcc

25

<210> SEQ ID NO 251  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 251

gtgctgcgat tacaggtgtg agc

23

<210> SEQ ID NO 252  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 252

tatgacagca gtattatact atcacc

26

<210> SEQ ID NO 253  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 253

ctggggacca aatctgaact gcc

23

<210> SEQ ID NO 254  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 254

gtagctattt ttatttccaa aaggagg

26

<210> SEQ ID NO 255  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 255

gcttgggacc ccaggacaag g

21

<210> SEQ ID NO 256  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 256

cctggccaac atggggaaat cc

22

<210> SEQ ID NO 257  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 257

aattgcttga acctgggagg tgg

23

<210> SEQ ID NO 258  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 258

gcctaagacc caaaagctat tagc

24

<210> SEQ ID NO 259  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 259

catattaaag ggcataattc aaattgg

27

<210> SEQ ID NO 260  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 260

ggatgttaacc agtgttatatc acagg

25

<210> SEQ ID NO 261  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 261

ggaagtttag tccacatctt ctacg

25

<210> SEQ ID NO 262  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 262

gcaccccacag gacaaccaca cg

22

<210> SEQ ID NO 263  
<211> LENGTH: 22

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 263

gggacgcgcc tggtaacaaa gg

22

<210> SEQ ID NO 264  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 264

gggcgtgggg ccacgctcc

19

<210> SEQ ID NO 265  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 265

cgcaaaagtg aagccctcct gg

22

<210> SEQ ID NO 266  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 266

gaaatcctac ttgatctaaa gtgagc

26

<210> SEQ ID NO 267  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 267

tttgagcaac ttggaaaaaa taagcg

26

<210> SEQ ID NO 268  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 268

ttccccaaag acaaatacgca cttcc

25

<210> SEQ ID NO 269  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 269

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ccatttgaa aatcacagtg aattcc

26

<210> SEQ ID NO 270  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 270

aaaaagaaaa ccctgaattc aaaagg

26

<210> SEQ ID NO 271  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 271

tgctgaaaag aagcatttaa aagtgg

26

<210> SEQ ID NO 272  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 272

ctcttaccag tttcagagct ttcc

24

<210> SEQ ID NO 273  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 273

tttcagcca aaaatcaagg acagg

25

<210> SEQ ID NO 274  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 274

cttgagccca ggagtttgag acc

23

<210> SEQ ID NO 275  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 275

cgccctgttagt accctctact agg

23

<210> SEQ ID NO 276  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 276
ggtaaaagaaa gaaggatttg aaaacc                                26

<210> SEQ ID NO 277
<211> LENGTH: 27
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 277
taagagtaat gaggttaaag tttatgc                                27

<210> SEQ ID NO 278
<211> LENGTH: 26
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 278
catttttatt gtcacaggcc atttgc                                26

<210> SEQ ID NO 279
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 279
gccacgcctt ctcttctgcc acc                                23

<210> SEQ ID NO 280
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 280
tgccctctcct gactgcactg tg                                22

<210> SEQ ID NO 281
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 281
ccatgctcta ccacgcccctt gg                                22

<210> SEQ ID NO 282
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 282
cattcaggct ggagtgcgggt gg                                22

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<210> SEQ ID NO 283  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 283

ctttaaaaatt gtctggctaa gacattg

27

<210> SEQ ID NO 284  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 284

ttgctcttgt tgcccggtt gg

22

<210> SEQ ID NO 285  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 285

gagcttagag gaaaagtatt atttcc

26

<210> SEQ ID NO 286  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 286

tggtgctgtg ccagacgctg g

21

<210> SEQ ID NO 287  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 287

cagatctttt tggctattgt cttgg

25

<210> SEQ ID NO 288  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 288

gaaggaaaagg gcctccccact gc

22

<210> SEQ ID NO 289  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 289

catgaaaaag catgctgggg agg

23

&lt;210&gt; SEQ ID NO 290

&lt;211&gt; LENGTH: 28

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 290

caaacataaa aaagcttaa tagaagcc

28

&lt;210&gt; SEQ ID NO 291

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 291

tcccaactat gaaaaatag aagacg

26

&lt;210&gt; SEQ ID NO 292

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 292

cacaattat ccgggcatgg tgg

23

&lt;210&gt; SEQ ID NO 293

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 293

tttccttac tgagtcttc taaagg

26

&lt;210&gt; SEQ ID NO 294

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 294

tgtccttga aatgttaggtt tgtgg

25

&lt;210&gt; SEQ ID NO 295

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 295

ggatcttgca atactgacat ctcc

24

&lt;210&gt; SEQ ID NO 296

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<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 296

atttgaaaag aactgaagga tctacc

26

<210> SEQ ID NO 297  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 297

gtgagctgag atctcgctc tgc

23

<210> SEQ ID NO 298  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 298

tttgtctgaa acagattcta aaagttgg

28

<210> SEQ ID NO 299  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 299

gcaggtgcct gtagtccag c

21

<210> SEQ ID NO 300  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 300

gttgagctt ctaaaattca tggattc

27

<210> SEQ ID NO 301  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 301

gtggtagtc aaaccgcaat tcc

23

<210> SEQ ID NO 302  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 302

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acccaaatcg acatatacgc tttgg 25

<210> SEQ ID NO 303  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 303

cacagaacgg atcctcaata aagg 24

<210> SEQ ID NO 304  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 304

gttaactcct cccttctt tatgg 25

<210> SEQ ID NO 305  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 305

gtgttcagag agcttgattt ccagg 25

<210> SEQ ID NO 306  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 306

cccaacttcat tttccaca tgg 23

<210> SEQ ID NO 307  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 307

atttatttag atgaagtgaa tattttcc 28

<210> SEQ ID NO 308  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 308

attttagttt gttttttttt agtgc 25

<210> SEQ ID NO 309  
<211> LENGTH: 24  
<212> TYPE: DNA

**157**

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 309

gtacagaagt gcttgatgca tacc

24

<210> SEQ ID NO 310  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 310

aggcagataaa aatttctcca tttagc

25

<210> SEQ ID NO 311  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 311

acaagcacga gccacagcac c

21

<210> SEQ ID NO 312  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 312

cgctttgtt gcccaggctg g

21

<210> SEQ ID NO 313  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 313

cccaaaaacag actttctaga taacc

25

<210> SEQ ID NO 314  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 314

ttcaaattgc ttttttctta ctcacc

26

<210> SEQ ID NO 315  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 315

gatctgaaaa aagtgacagg ttgg

24

**158**

<210> SEQ ID NO 316  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 316

cactgaaatt tgaaaggaac atatgg

26

<210> SEQ ID NO 317  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 317

tctggtgtag tggcctctag g

21

<210> SEQ ID NO 318  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 318

accataagtg gtttacctg atgg

24

<210> SEQ ID NO 319  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 319

cccaaggcgca ggtgattctc c

21

<210> SEQ ID NO 320  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 320

ggtgtggctcac gcctgaaatc c

21

<210> SEQ ID NO 321  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 321

cacagtccac gtgccacaat cc

22

<210> SEQ ID NO 322  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 322

aatcatgtta acacatccct ctcc

24

&lt;210&gt; SEQ ID NO 323

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 323

gaagagagtg ttgaaaggaa aagc

24

&lt;210&gt; SEQ ID NO 324

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 324

cgagaccata ctggctaaga tgg

23

&lt;210&gt; SEQ ID NO 325

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 325

attagccaca caataaatgt tctgg

25

&lt;210&gt; SEQ ID NO 326

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 326

tttgaaaagc gttgcaatat gatgc

25

&lt;210&gt; SEQ ID NO 327

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 327

ggttgcagtg agccgagatc g

21

&lt;210&gt; SEQ ID NO 328

&lt;211&gt; LENGTH: 20

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 328

ggtgggagga ctgcctgagc

20

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<210> SEQ ID NO 329  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 329

aacagagaga aaaaacacaa attacc

26

<210> SEQ ID NO 330  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 330

gatatctaga attcccaaat acttgg

26

<210> SEQ ID NO 331  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 331

gtgatagaat taaaggaaaa aataaacg

28

<210> SEQ ID NO 332  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 332

attgttcctt ttctaaatat tctacc

26

<210> SEQ ID NO 333  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 333

cagcactttg ggaggctgag g

21

<210> SEQ ID NO 334  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 334

cacagaggtt tcacagtgct gg

22

<210> SEQ ID NO 335  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 335

aacttctgct tctgtccata atgc

24

<210> SEQ ID NO 336  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 336

gcctgtataatc ccagcacattt gg

22

<210> SEQ ID NO 337  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 337

gccagtaaac atatgaaaag gtgc

24

<210> SEQ ID NO 338  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 338

aattatgtaa ataaagagtg aaaagg

26

<210> SEQ ID NO 339  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 339

cccctacaca gaaaaaaca ttcc

24

<210> SEQ ID NO 340  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 340

tgagtgtcaa agaaaaatac aattgg

26

<210> SEQ ID NO 341  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 341

atacacagag aaaatgagtc cacc

24

<210> SEQ ID NO 342  
<211> LENGTH: 23

**167**

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 342

aacactcccc ttctctgttt agc

23

<210> SEQ ID NO 343  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 343

gatattcttt gcaaccttagg atgc

24

<210> SEQ ID NO 344  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 344

ctctaaaact aatcagcaat gtaacc

26

<210> SEQ ID NO 345  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 345

cacctgtaat cccagcactt tgg

23

<210> SEQ ID NO 346  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 346

cgtaaaaactg ccacaaagct tgtagg

26

<210> SEQ ID NO 347  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 347

gtggcagagg tgcaagcaag c

21

<210> SEQ ID NO 348  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 348

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acagaaaatga caaacgcatt tacc

24

<210> SEQ ID NO 349  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 349

acactcttctt agctaggctt tgg

23

<210> SEQ ID NO 350  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 350

gagcttgaa tagggcagtt cc

22

<210> SEQ ID NO 351  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 351

ctgggttctt taaacatgtc cagg

24

<210> SEQ ID NO 352  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 352

tcaagaagg acactgcagt ggc

23

<210> SEQ ID NO 353  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 353

catgcacaca aactatctca ttcc

24

<210> SEQ ID NO 354  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 354

tagccgggca tggtggcacg

20

<210> SEQ ID NO 355  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 355

atcatgctga ttgaatttca aatagc

26

<210> SEQ ID NO 356  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 356

ttggcatgca gggcagtgac c

21

<210> SEQ ID NO 357  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 357

gttgttgaga taataaacacc tgc

23

<210> SEQ ID NO 358  
 <211> LENGTH: 27  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 358

ttgctatata ataatcattt gtgatcc

27

<210> SEQ ID NO 359  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 359

cggtaactgt tactctggaa tgg

23

<210> SEQ ID NO 360  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 360

aggcttagtt cccttcttcc cc

22

<210> SEQ ID NO 361  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 361

gtagtgccta gcacagagaa agc

23

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<210> SEQ ID NO 362  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 362

ctagcctggg caacaagagc g

21

<210> SEQ ID NO 363  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 363

tctctctccct ctctggatc ag

22

<210> SEQ ID NO 364  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 364

gtttgaatat ttgtatgcag caagc

25

<210> SEQ ID NO 365  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 365

tagaacaataat tctggcttat aaaagc

26

<210> SEQ ID NO 366  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 366

ccactctacc tttattccctt gcc

23

<210> SEQ ID NO 367  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 367

agaccagaat atgcaagcag agg

23

<210> SEQ ID NO 368  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 368

ggacgttttg ctgggtctg cg

22

<210> SEQ ID NO 369  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 369

aaggaacaaa ctgttgtcac atgc

24

<210> SEQ ID NO 370  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 370

atgttagctgg gactacaggc gc

22

<210> SEQ ID NO 371  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 371

ggctcatgcc tgtaatccca gc

22

<210> SEQ ID NO 372  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 372

atgagggttt cacacaaaaa gatgc

25

<210> SEQ ID NO 373  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 373

tgggcgacag agcaagactc c

21

<210> SEQ ID NO 374  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 374

aaatgtccct aaaagtgtatc aacagc

26

&lt;210&gt; SEQ ID NO 375

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<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 375

cagactcagt tttacctcat cagc

24

<210> SEQ ID NO 376  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 376

agtgatctt cctcttaac ctcc

24

<210> SEQ ID NO 377  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 377

ccagctattc aggaggccaa gg

22

<210> SEQ ID NO 378  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 378

cttaaacatt atgacactgt cttgc

25

<210> SEQ ID NO 379  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 379

ccaggcttat gagggcgttc c

21

<210> SEQ ID NO 380  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 380

tccaaagcat ccctacatta tacc

24

<210> SEQ ID NO 381  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 381

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acatacatac atgcagtgac tagc 24

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<210> SEQ ID NO 382
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 382

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tacaggtgcc agccaccatg c 21

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<210> SEQ ID NO 383
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 383

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gctctgtatc ccagcactct gg 22

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<210> SEQ ID NO 384
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 384

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gacagagtcc cactttgtt gc 22

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<210> SEQ ID NO 385
<211> LENGTH: 22
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 385

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gtgccttcca aagcagtgtta gg 22

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<210> SEQ ID NO 386
<211> LENGTH: 25
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 386

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tatcttactg ggtatgtata atgcc 25

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<210> SEQ ID NO 387
<211> LENGTH: 23
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 387

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caaaggaaat acgtcctacc agg 23

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<210> SEQ ID NO 388
<211> LENGTH: 23
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 388

ccttttctca cagacatgct tcc

23

<210> SEQ ID NO 389  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 389

taaacacagt gaggagaatc cc

22

<210> SEQ ID NO 390  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 390

ataaaagcaaa cttctaaaag ggtcc

25

<210> SEQ ID NO 391  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 391

accactacac tccagcctgg g

21

<210> SEQ ID NO 392  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 392

gatacctggg tcagagtaag tgc

23

<210> SEQ ID NO 393  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 393

tgtaatctca gctacttggg agg

23

<210> SEQ ID NO 394  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 394

gtgtcggttt ctcttcctct acg

23

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<210> SEQ ID NO 395  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 395

ctggctagta tgagggttgt gc

22

<210> SEQ ID NO 396  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 396

ggactagcca catttcaacc agg

23

<210> SEQ ID NO 397  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 397

gcagtatact gagaattttag tttcc

25

<210> SEQ ID NO 398  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 398

gaggctgagg caggagaatg g

21

<210> SEQ ID NO 399  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 399

cattgttga tgaaggtaaa cagc

24

<210> SEQ ID NO 400  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 400

cagacaagag tggctacggc ag

22

<210> SEQ ID NO 401  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 401

acgcccagcc agattattca gg

22

&lt;210&gt; SEQ ID NO 402

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 402

ggaaccagaa agaagtgc aa agg

23

&lt;210&gt; SEQ ID NO 403

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 403

tgagccatct tggaggcagg c

21

&lt;210&gt; SEQ ID NO 404

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 404

caggaccc tcataaacct cc

22

&lt;210&gt; SEQ ID NO 405

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 405

aacacaacat atctgacc tt acgc

24

&lt;210&gt; SEQ ID NO 406

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 406

gccttagaag tccagaggaa agc

23

&lt;210&gt; SEQ ID NO 407

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 407

tgacgtaccc agtagaccc tt cc

22

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<210> SEQ ID NO 408  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 408

ctctgcaagc ctggaaaca gg

22

<210> SEQ ID NO 409  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 409

gccttgtccc caagtcccaa gg

22

<210> SEQ ID NO 410  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 410

gcaaaggac tcctgaaatt cc

22

<210> SEQ ID NO 411  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 411

gctcctgcct gtaatcccg c

21

<210> SEQ ID NO 412  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 412

gaaggaaaaca gaaaaagcag aggc

24

<210> SEQ ID NO 413  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 413

cttactaccg ttcttttca ctgg

24

<210> SEQ ID NO 414  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 414

actattctgt ttcttttaggt ttactgc

27

<210> SEQ ID NO 415  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 415

cggtgtggctca cacctgtaat cc

22

<210> SEQ ID NO 416  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 416

agccagagtt ctgtgtctca gg

22

<210> SEQ ID NO 417  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 417

taatttgcac ttctgtgccgc tcc

23

<210> SEQ ID NO 418  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 418

cactttaat acagatccca atagg

25

<210> SEQ ID NO 419  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 419

atgtatTTTT tcttttcctg tcaagg

26

<210> SEQ ID NO 420  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 420

aaatgttaac attattctcc ctaagg

26

<210> SEQ ID NO 421  
<211> LENGTH: 22

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 421

catatggcca gatcccggtct cc

22

<210> SEQ ID NO 422  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 422

acagggtgtga gccgcgtgcac c

21

<210> SEQ ID NO 423  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 423

gccaaggacgt ttacagtttt ggc

23

<210> SEQ ID NO 424  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 424

aggaaaacttc tgaggatgtat ggg

23

<210> SEQ ID NO 425  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 425

gctttataagg gcagtctgaa ttcc

24

<210> SEQ ID NO 426  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 426

ttagaataaaa agtttatctcg ggagg

25

<210> SEQ ID NO 427  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 427

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taatttcttc agctttatcc ctcag

25

<210> SEQ ID NO 428  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 428

cacatgacta attctctatt cattcc

26

<210> SEQ ID NO 429  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 429

aaagacctca agaaaagagt cacc

24

<210> SEQ ID NO 430  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 430

gaccctataaa gattatatgc ccag

24

<210> SEQ ID NO 431  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 431

aaagtactaa tgcagtgtgt cagc

24

<210> SEQ ID NO 432  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 432

gagggttcctc gattccccctg c

21

<210> SEQ ID NO 433  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 433

ggagagcaga ggaattcaca gg

22

<210> SEQ ID NO 434  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 434

agtaattaga aactgattct aagacg

26

<210> SEQ ID NO 435

<211> LENGTH: 23

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 435

cataccattg ccaatccagt tcc

23

<210> SEQ ID NO 436

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 436

attacgggtg octgccactg c

21

<210> SEQ ID NO 437

<211> LENGTH: 21

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 437

cagccaggca gaggagagag g

21

<210> SEQ ID NO 438

<211> LENGTH: 25

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 438

tttcattcc aagttctgt ttggg

25

<210> SEQ ID NO 439

<211> LENGTH: 26

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 439

tttcaaatacg aatggat aatccc

26

<210> SEQ ID NO 440

<211> LENGTH: 22

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 440

taagccgaga tcacaccact gc

22

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<210> SEQ ID NO 441  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 441

ccttcagcgc attatatctt ggc

23

<210> SEQ ID NO 442  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 442

ccatctaatac catcttaaat tcacc

25

<210> SEQ ID NO 443  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 443

gagtggagac tgcgccactg c

21

<210> SEQ ID NO 444  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 444

aatcatgtgc caattaaacc atggc

25

<210> SEQ ID NO 445  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 445

cccagggacc agaccagacc

20

<210> SEQ ID NO 446  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 446

ctcactcacc agtgaaaatc agc

23

<210> SEQ ID NO 447  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 447

ggttgtctc gaactcctga cc

22

&lt;210&gt; SEQ ID NO 448

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 448

gttcccccaag ctcctttctg c

21

&lt;210&gt; SEQ ID NO 449

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 449

agaaagatgt agaagggtcc agc

23

&lt;210&gt; SEQ ID NO 450

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 450

ggaaaaagggt gtattatgca agcg

24

&lt;210&gt; SEQ ID NO 451

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 451

ctctctcaga cctaattgcaa aagc

24

&lt;210&gt; SEQ ID NO 452

&lt;211&gt; LENGTH: 27

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 452

aactatacat acagtatttg tatttagc

27

&lt;210&gt; SEQ ID NO 453

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 453

aaatataatgc aatccatgtat ccagg

25

&lt;210&gt; SEQ ID NO 454

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<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 454

ctttctccac tctaagagaa ccc

23

<210> SEQ ID NO 455  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 455

ttttggtgtg ttcatattgg ctgc

24

<210> SEQ ID NO 456  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 456

gcttccacaa atgacagaca aagg

24

<210> SEQ ID NO 457  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 457

ggctcatgct tgtatccca gc

22

<210> SEQ ID NO 458  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 458

catatgaatt gttgttcctt tgtagg

26

<210> SEQ ID NO 459  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 459

cactggtaca agtccaagag tcc

23

<210> SEQ ID NO 460  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 460

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gaccctgtgt ctacttcctg gg 22

<210> SEQ ID NO 461  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 461

tatttgaact atctttgaa atgtcc 26

<210> SEQ ID NO 462  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 462

ctgattaaaa agtattaccc ttggc 25

<210> SEQ ID NO 463  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 463

tttgaaactg cactcaataa cttgg 25

<210> SEQ ID NO 464  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 464

agtaatgtgt catgatccaa tggc 24

<210> SEQ ID NO 465  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 465

gaaagcattt cccaatgtct cacc 24

<210> SEQ ID NO 466  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 466

caatggacaa aaggcccaac tgc 23

<210> SEQ ID NO 467  
<211> LENGTH: 24  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 467

tccagctctg gctttttgt taag

24

<210> SEQ ID NO 468  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 468

acggagtctc actccgtgac c

21

<210> SEQ ID NO 469  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 469

ctatgtcata gtcaagagac tttgc

25

<210> SEQ ID NO 470  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 470

gttcaaggcgta ttctcctgtc tcg

23

<210> SEQ ID NO 471  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 471

ccacctaata cttaaatacg gaagc

25

<210> SEQ ID NO 472  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 472

atattcaaca aacttaatacg tgaagtgc

27

<210> SEQ ID NO 473  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 473

ttacaggcgt gagtcaccat gc

22

<210> SEQ ID NO 474  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 474

aacacacctcca agaggccaaa cg

22

<210> SEQ ID NO 475  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 475

tactattggc aaatttcaat tataatgg

27

<210> SEQ ID NO 476  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 476

agccccacatc ctaaaattca ataag

25

<210> SEQ ID NO 477  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 477

gaaaagtggat aagtgttgt ctgg

24

<210> SEQ ID NO 478  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 478

ggccaggcat tcaagaccag c

21

<210> SEQ ID NO 479  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 479

agcccaacaac aaaaagacac aacc

24

<210> SEQ ID NO 480  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 480

ttgagccccag gagttcaaga cc

22

&lt;210&gt; SEQ ID NO 481

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 481

cagactaaag atctcagaga gaaac

25

&lt;210&gt; SEQ ID NO 482

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 482

cgcttgtaat cccagcactt gg

22

&lt;210&gt; SEQ ID NO 483

&lt;211&gt; LENGTH: 25

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 483

aaaagtgaaa tcagaatttg tttcc

25

&lt;210&gt; SEQ ID NO 484

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 484

caggcgtgag caactgtgtc c

21

&lt;210&gt; SEQ ID NO 485

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 485

ggtcccgtag gatctcggtt gc

22

&lt;210&gt; SEQ ID NO 486

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 486

actttgaaaa tggttgtata gctggg

26

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<210> SEQ ID NO 487  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 487

ttccctgcat ctaagtcttc tcc

23

<210> SEQ ID NO 488  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 488

agatatatctac cattgaagag tttgc

25

<210> SEQ ID NO 489  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 489

agtcttcaact tcactttgtt gtcc

24

<210> SEQ ID NO 490  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 490

ccatgcaggat atgaaaataaa aaagc

25

<210> SEQ ID NO 491  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 491

tgggtgacag agtgagactc c

21

<210> SEQ ID NO 492  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 492

acagcaatac cgggttaaca tgc

23

<210> SEQ ID NO 493  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 493

tttatgtaaa agatgaatgc gaggc

25

<210> SEQ ID NO 494  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 494

ctactctgct actggaaaca gg

22

<210> SEQ ID NO 495  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 495

caaacgttag tctggcaaaa tgcg

24

<210> SEQ ID NO 496  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 496

tgcacgctac cacaccaggc

20

<210> SEQ ID NO 497  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 497

aattcttggaa tctgtgttt tactgc

26

<210> SEQ ID NO 498  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 498

taccagttat cattctttt ctgc

24

<210> SEQ ID NO 499  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 499

atccacccac ctggcctcc

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<210> SEQ ID NO 500  
<211> LENGTH: 22

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 500

cactctgcct ggcccttaat gg

22

<210> SEQ ID NO 501  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 501

atagtttgtt taatatgccca ctaagg

26

<210> SEQ ID NO 502  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 502

cggtgagcca ccgcacacctgg

20

<210> SEQ ID NO 503  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 503

ctccatcaca caaattttat gtggc

25

<210> SEQ ID NO 504  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 504

agacggagtc tcgttctgtc gc

22

<210> SEQ ID NO 505  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 505

tcccaggttc aagccattct cc

22

<210> SEQ ID NO 506  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 506

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tatTTTgaga gtctcactct gtcg

24

<210> SEQ ID NO 507  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 507

gtctcgaaCT cctgacCTCA gg

22

<210> SEQ ID NO 508  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 508

aaggaggtGA agagtGAact acg

23

<210> SEQ ID NO 509  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 509

gtctcaggTT ttggacttAC ttgg

24

<210> SEQ ID NO 510  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 510

tttacAGATC ttAAATGCA ttagGAC

26

<210> SEQ ID NO 511  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 511

gtacACTGAA caaaggAGAC agg

23

<210> SEQ ID NO 512  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 512

ctggTAGTAA tgcaAAATAG cacc

24

<210> SEQ ID NO 513  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 513

catttaatgt gaaatgaatt ataagcc

27

<210> SEQ ID NO 514  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 514

gagacagggt ttcactatgt tgg

23

<210> SEQ ID NO 515  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 515

ccagcacttt ggaaggctga gg

22

<210> SEQ ID NO 516  
 <211> LENGTH: 25  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 516

gaaaccaagt atcatggtaa attgc

25

<210> SEQ ID NO 517  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 517

cagtgagggc tgctcagttc c

21

<210> SEQ ID NO 518  
 <211> LENGTH: 20  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 518

gccaggtgcg gtggctcacg

20

<210> SEQ ID NO 519  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 519

catgcctgta atcccagcta cc

22

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<210> SEQ ID NO 520  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 520

atgttaaatgg tacagtcact ttagg

25

<210> SEQ ID NO 521  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 521

cccacacaatac agagaactct tacc

24

<210> SEQ ID NO 522  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 522

tgaaacatgc agcccagtgt cc

22

<210> SEQ ID NO 523  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 523

tgttttttct cctgccttca atcc

24

<210> SEQ ID NO 524  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 524

gttttcctgg gtctccatct gg

22

<210> SEQ ID NO 525  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 525

gcagcccgctt gaaaaacaaaaa cagc

24

<210> SEQ ID NO 526  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 526

gatcacgtta cattttgggg tgg

23

&lt;210&gt; SEQ ID NO 527

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 527

tagggctgaaa aactaaaatt tggc

26

&lt;210&gt; SEQ ID NO 528

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 528

ctcccttggg ctccctttagt cc

22

&lt;210&gt; SEQ ID NO 529

&lt;211&gt; LENGTH: 20

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 529

gcctcgccct cccaaagtgc

20

&lt;210&gt; SEQ ID NO 530

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 530

aatgcctaga gagattggc agg

23

&lt;210&gt; SEQ ID NO 531

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 531

gagatgggggt ttcactatgt tgg

23

&lt;210&gt; SEQ ID NO 532

&lt;211&gt; LENGTH: 22

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 532

tgtgatcttg ccactgcact cc

22

&lt;210&gt; SEQ ID NO 533

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<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 533

acttcttc cattgtttc ttcc

24

<210> SEQ ID NO 534  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 534

cggtccccggg ctcagttcta c

21

<210> SEQ ID NO 535  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 535

ccaaaaacaat aaaatcacaa tttgggg

26

<210> SEQ ID NO 536  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 536

ctgaactgcc ttagagtaaa tccg

24

<210> SEQ ID NO 537  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 537

atttctgtat caggctgtg ttcc

24

<210> SEQ ID NO 538  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 538

ggctgacccc ttcaactgttt cc

22

<210> SEQ ID NO 539  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 539

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caaaaattag ccaggcatgg tgg 23

<210> SEQ ID NO 540  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 540

gcagttagca gtgatcgac c 21

<210> SEQ ID NO 541  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 541

aaagactgtg aactaacttg tttgc 25

<210> SEQ ID NO 542  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 542

tgcacaagaat tacacattat taggc 25

<210> SEQ ID NO 543  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 543

ggccaggatg tcattaactt tcc 23

<210> SEQ ID NO 544  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 544

gtaagagctg acgtgtattc tgc 23

<210> SEQ ID NO 545  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 545

cccggtgagg ccgcacatcc 20

<210> SEQ ID NO 546  
<211> LENGTH: 20  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 546  
cctgcgcctt aacccttc

20

<210> SEQ ID NO 547  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 547  
cggcgccatg gggccatcg

19

<210> SEQ ID NO 548  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 548  
acttaaggaa acgaacatga cacc

24

<210> SEQ ID NO 549  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 549  
gagaccgagt cttgtgtgt cg

22

<210> SEQ ID NO 550  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 550  
gtattaattt aagatgattt ggaatgc

27

<210> SEQ ID NO 551  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 551  
tctttaaaag actatcgctg agg

24

<210> SEQ ID NO 552  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 552  
aaaaagagaca tcagtagagc atcc

24

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<210> SEQ ID NO 553  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 553

gttcatgttt tctttgacgt ctcc

24

<210> SEQ ID NO 554  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 554

tttcgaaagt tcaggctgag tgc

23

<210> SEQ ID NO 555  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 555

gaccctcaaa acaatcctct aagg

24

<210> SEQ ID NO 556  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 556

caaaaacacac ttagaaacaa actgc

25

<210> SEQ ID NO 557  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 557

gcctggcgca catagtgaga cc

22

<210> SEQ ID NO 558  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 558

ggcaggagaa tggcgtgaac c

21

<210> SEQ ID NO 559  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 559

tttgctcggtt gcccaggctg g

21

&lt;210&gt; SEQ ID NO 560

&lt;211&gt; LENGTH: 26

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 560

gcaacttaat gtgatagaat aatagc

26

&lt;210&gt; SEQ ID NO 561

&lt;211&gt; LENGTH: 20

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 561

cctcccccttc tgctgccagc

20

&lt;210&gt; SEQ ID NO 562

&lt;211&gt; LENGTH: 24

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 562

ccacaacaat gtaaaactcct ctgg

24

&lt;210&gt; SEQ ID NO 563

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 563

tactctccct agagttcggtt ccc

23

&lt;210&gt; SEQ ID NO 564

&lt;211&gt; LENGTH: 21

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 564

gggtccccct ttggccattc c

21

&lt;210&gt; SEQ ID NO 565

&lt;211&gt; LENGTH: 23

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 565

gatcttggct cacttcaacc tcc

23

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<210> SEQ ID NO 566  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 566

aggggaaata tttaaacctt gg

22

<210> SEQ ID NO 567  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 567

aatgcaatgg tgcatttaca gagg

24

<210> SEQ ID NO 568  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 568

tcattttac tatttctaca tggtcc

26

<210> SEQ ID NO 569  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 569

ggaaggggaaa tgcccatgaa cc

22

<210> SEQ ID NO 570  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 570

agtgaacatt ttctgcagcc tcc

23

<210> SEQ ID NO 571  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 571

caacaggacg tcaggcgatc c

21

<210> SEQ ID NO 572  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 572

ccttcaggct gtcctgaaaa gg

22

<210> SEQ ID NO 573  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 573

agtctcaactc catcgcccaag g

21

<210> SEQ ID NO 574  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 574

actgtgaaca gtagttaact cagg

24

<210> SEQ ID NO 575  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 575

gcatgcctgt aatccaagct gc

22

<210> SEQ ID NO 576  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 576

gaaacaattc tctttcaca cttgc

25

<210> SEQ ID NO 577  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 577

ggctcatgcc tgttatccca gc

22

<210> SEQ ID NO 578  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 578

agaagaagct tagtcatatg tttgg

25

<210> SEQ ID NO 579  
<211> LENGTH: 24

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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 579

cagatgcttg agccaaacaa atgg

24

<210> SEQ ID NO 580  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 580

ctggcagaca gagtgagact cc

22

<210> SEQ ID NO 581  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 581

aatgtgtcaa tattattcat tacaggg

27

<210> SEQ ID NO 582  
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<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 582

gcaggagaat tgcttgaacc tgg

23

<210> SEQ ID NO 583  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 583

cttagtcaa attaaaacag tctatcc

27

<210> SEQ ID NO 584  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 584

gatttctatac tcctgcaacc acc

23

<210> SEQ ID NO 585  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 585

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ttcttgta actactaaaa atctcc

26

<210> SEQ ID NO 586  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 586

aaagggtctt cataaggcta atgg

24

<210> SEQ ID NO 587  
<211> LENGTH: 27  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 587

ctcttaagga ttatttatata gaagacc

27

<210> SEQ ID NO 588  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 588

caggaggagc cccagagc

18

<210> SEQ ID NO 589  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 589

tcctggggat gggtggatgc

20

<210> SEQ ID NO 590  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 590

tgacccca gagtttacac agc

23

<210> SEQ ID NO 591  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 591

agtcaaggca ggctctgcc

19

<210> SEQ ID NO 592  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 592

tatTTggcc ccatccagaa agc

23

<210> SEQ ID NO 593  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 593

caccaggagt acagcttgt tcc

23

<210> SEQ ID NO 594  
 <211> LENGTH: 19  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 594

gaggagcccc agagcctgc

19

<210> SEQ ID NO 595  
 <211> LENGTH: 22  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 595

tggggatgg tggatgctta cc

22

<210> SEQ ID NO 596  
 <211> LENGTH: 23  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 596

cccacagagt ttacacagct tgc

23

<210> SEQ ID NO 597  
 <211> LENGTH: 19  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 597

caggctctgc ccactcacc

19

<210> SEQ ID NO 598  
 <211> LENGTH: 21  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 598

ccatccagaa agcccaaagc c

21

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<210> SEQ ID NO 599  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 599

ccagagtaca gctttgttcc tcattc

26

<210> SEQ ID NO 600  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 600

gcagtgacaaa caacgcacag cg

22

<210> SEQ ID NO 601  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 601

ctgccaccct ccacagtccc

20

<210> SEQ ID NO 602  
<211> LENGTH: 18  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 602

gccaagacca tgcatgcg

18

<210> SEQ ID NO 603  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 603

cccaggggaca aagagactcc c

21

<210> SEQ ID NO 604  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

<400> SEQUENCE: 604

caggaaggcag acagtcttct agttcc

26

<210> SEQ ID NO 605  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

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&lt;400&gt; SEQUENCE: 605

tgccctgtataat cccaaacactt tgg

23

<210> SEQ ID NO 606  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 606

tcacctctggc caggatggg

19

<210> SEQ ID NO 607  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 607

atggggaaatg ggagtaggaa gc

22

<210> SEQ ID NO 608  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 608

cagatcagtt ctccccctcca gc

22

<210> SEQ ID NO 609  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 609

acaaaaaaaga aacatgctca gagagg

26

<210> SEQ ID NO 610  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 610

tggtgtggcatg catctgtatg cc

22

<210> SEQ ID NO 611  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 611

agggtgcata tagatgttagt catccc

26

&lt;210&gt; SEQ ID NO 612

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<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 612

ccaggacagg atggagatct gg

22

<210> SEQ ID NO 613  
<211> LENGTH: 24  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 613

agggAACCTG TGCATTATCC TTGC

24

<210> SEQ ID NO 614  
<211> LENGTH: 25  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 614

cagaagtctt gctttaagga ggagg

25

<210> SEQ ID NO 615  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 615

gggtacgtga aactcaccaa gg

22

<210> SEQ ID NO 616  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 616

cagagtgtgg caagcaaggg

20

<210> SEQ ID NO 617  
<211> LENGTH: 28  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 617

aacattttaa aggtacaaat aacgtggg

28

<210> SEQ ID NO 618  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 618

tagggagcaa cagccattaa gc

22

<210> SEQ ID NO 619  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 619

ggtgtcactgt ccagctctgg

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<210> SEQ ID NO 620  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 620

actctcgctg aactcgccctg g

21

<210> SEQ ID NO 621  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 621

ctcggtctct ggtggtaacgc

20

<210> SEQ ID NO 622  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 622

gcaagaggc cgagctggg

19

<210> SEQ ID NO 623  
<211> LENGTH: 26  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 623

ggaagaagtg aaacaagaga tgaagg

26

<210> SEQ ID NO 624  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide

&lt;400&gt; SEQUENCE: 624

cccagagaac aaaccggatt agg

23

<210> SEQ ID NO 625  
<211> LENGTH: 23  
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 625

cccttcaacc ttctccaatc tgc

23

<210> SEQ ID NO 626  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 626

cccatgtcca gtggtttagg g

21

<210> SEQ ID NO 627  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 627

gagattggtg ggagacagat gg

22

<210> SEQ ID NO 628  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 628

cttctcagct caaagtcca gcg

23

<210> SEQ ID NO 629  
<211> LENGTH: 22  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 629

gaatgggaga gatgaccaga gg

22

<210> SEQ ID NO 630  
<211> LENGTH: 20  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 630

aaggcaagg gggtatgtgg

20

<210> SEQ ID NO 631  
<211> LENGTH: 21  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 631

&lt;400&gt; SEQUENCE: 631

ggaaggaaagc atggaaacac c

21

<210> SEQ ID NO 632  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 632  
ccatcaatgc tctgtctgtc tgg

23

<210> SEQ ID NO 633  
<211> LENGTH: 19  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 633  
gtgccgtgac tgtgcttgg

19

<210> SEQ ID NO 634  
<211> LENGTH: 23  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Synthetic oligonucleotide  
<400> SEQUENCE: 634  
acatcccatt gacctcatca agc

23

The invention claimed is:

1. A method of identifying a gene breakpoint, said method comprising:

- (i) in a first round amplification reaction, contacting a DNA sample with:
    - (a) one or more forward primers directed to the antisense strand of a genomic DNA region of the flanking gene or fragment thereof, said region being located 5' relative to the gene breakpoint; and
    - (b) one or more reverse primers directed to the sense strand of a genomic DNA region of the flanking gene or fragment thereof, said region being located 3' relative to the gene breakpoint;
- wherein all of the forward primers or all of the reverse primers or all of both the forward and reverse primers are operably linked at their 5' end to an oligonucleotide tag; and
- if the forward primers are operably linked to an oligonucleotide tag then the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (i)(a);
- if the reverse primers are operably linked to an oligonucleotide tag then the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (i)(b);
- if both the forward primers and the reverse primers are operably linked to an oligonucleotide tag then forward primer oligonucleotide tags are different relative to the reverse primer tags; and
- (c) if a forward primer tag is present then hybridizing a primer directed to the forward primer oligonucleotide tag of step (i)(a); and
- (d) if a reverse primer tag is present then hybridizing a primer directed to the reverse primer oligonucleotide tag of step (i)(b);

- (ii) amplifying the DNA sample of step (i);
  - (iii) in a second round amplification reaction, contacting the amplicon generated in step (ii) with:
    - (a) one or more forward primers directed to the antisense strand of a genomic DNA region of the flanking gene or fragment thereof, said region being located 5' relative to the gene breakpoint and 3' relative to one or more of the regions of step (i)(a); and
    - (b) one or more reverse primers directed to the sense strand of a genomic DNA region of the flanking gene or fragment thereof, said region being located 3' to the gene breakpoint and 5' relative to one or more of the regions of step (i)(b);
- wherein all of the forward primers or all of the reverse primers or all of both the forward and reverse primers are operably linked at their 5' end to an oligonucleotide tag; and
- if the forward primers are operably linked to an oligonucleotide tag then the oligonucleotide tags of the forward primers are the same relative to the forward primer tags of step (iii)(a);
- if the reverse primers are operably linked to an oligonucleotide tag then the oligonucleotide tags of the reverse primers are the same relative to the reverse primer tags of step (iii)(b);
- if both the forward primers and the reverse primers are operably linked to an oligonucleotide tag then forward primer oligonucleotide tags are different relative to the reverse primer tags and which forward and reverse primer tags of step (iii) are different relative to the forward and reverse primer tags of step (i); and
- (c) if a forward primer tag is present then hybridizing a primer directed to the forward primer oligonucleotide tag of step (iii)(a); and

257

- (d) if a reverse primer tag is present then hybridizing a primer directed to the reverse primer oligonucleotide tag of step (iii)(b);
- (iv) amplifying the DNA sample of step (iii); and
- (v) analysing the amplified DNA.

2. The method according to claim 1 wherein:

- (i) one primer is used in step (i)(a) and 24-400 primers are used in step (i)(b); or
- (ii) one primer is used in step (i)(b) and two or more primers are used in step (i)(a).

3. The method according to claim 1 wherein:

- (i) one primer is used in step (iii)(a) and 24-400 primers are used in step (iii)(b); or
- (ii) one primer is used in step (iii)(b) and two or more primers are used in step (iii)(a).

4. The method according to claim 1 wherein said gene breakpoint is a homologous recombination point or said gene translocation breakpoint is a chromosomal gene translocation breakpoint.

5. The method according to claim 4 wherein said gene translocation breakpoint is selected from:

- (i) BCR-ABL translocation
- (ii) PML-RAR $\alpha$  translocation
- (iii) t(2;5)(p23;q35) translocation
- (iv) t(8;14) translocation
- (v) t(9;22)(q34;q11) translocation
- (vi) t(11;14) translocation
- (vii) t(11;22)(q24;q11.2-12) translocation
- (viii) t(14;18)(q32;q21) translocation
- (ix) t(17;22) translocation
- (x) t(15;17) translocation
- (xi) t(1;12) (q21;p13) translocation
- (xii) t(9;12)(p24;p13) translocation
- (xiii) t(X;18)(p11.2;q11.2) translocation
- (xiv) t(1;11)(q42.1;q14.3) translocation
- (xv) t(1;19) translocation.

6. The method according to claim 1 wherein 1-30 primers are used in step (i)(a) and 24-400 primers are used in step (i)(b).

258

7. The method according to claim 1 wherein 1-30 primers are used in step (iii)(a) and 24-400 primers are used in step (iii)(b).

8. The method according to claim 1 wherein said amplified DNA of step (iv) is subjected to a further step of amplification, selection or enrichment.

9. The method according to claim 1 wherein said gene breakpoint is a chromosomal BCR-ABL translocation and:

- (a) the forward primers of step (i)(a) have the nucleic acid sequences of SEQ ID NOS:10-15;
- (b) the reverse primers of step (i)(b) have the nucleic acid sequences of SEQ ID NOS:23-304 and are linked to the oligonucleotide tag having the nucleic acid sequence of SEQ ID NO:22;
- (c) the forward primers of step (iii)(a) have the nucleic acid sequences of SEQ ID NOS:16-21; and
- (d) the reverse primers of step (iii)(b) have the nucleic acid sequences of SEQ ID NOS:306-587 and are linked to the oligonucleotide tag having the nucleic acid sequence of SEQ ID NO:305.

10. The method according to claim 1 wherein said gene breakpoint is a chromosomal PML-RAR $\alpha$  translocation and:

- 25 (a) the forward primers of step (i)(a) have the nucleic acid sequences of SEQ ID NOS:588-593; and
- (b) the reverse primers of step (i)(b) have the nucleic acid sequences of SEQ ID NOS:601-634 and are linked to the oligonucleotide tag having the nucleic acid sequence of SEQ ID NO:22

30 and wherein step (ii) is followed by bottleneck PCR which is performed using primers having the nucleic acid sequences of SEQ ID NOS:594-599.

11. The method according to claim 8, wherein either the forward primers or the reverse primers of step (iii)(a) or (b) have been designed or are used under conditions wherein they do not hybridize and extend efficiently.

\* \* \* \* \*